

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 29, 2003, 09:51:49 ; Search time 2055 Seconds
(without alignments)
1596.644 Million cell updates/sec

Title: US-09-866-582A-2
Perfect score: 661
Sequence: 1 MDAAVDRGVYDEDFHVRILD.....GEOELMIQKLSRSSGAAYV 135

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Xgapop 10.0 , Xgapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Command line parameters:

-MODEL=frame+P2n model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_P/US09866582/runat_27082003_095333_9839/app_query.fasta.1.327
-DB=EST -QFMT=fastcap -SUFFIX=1st -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=100
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=50 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09866582@cgn.1.1.2874 @runat_27082003_095333_9839 -NCPU=6 -ICPU=3
-NO_MMAP -LARGESQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	577	87.3	466	9	AV392837	AV392837 AV392837
2	227	34.3	493	10	BE352290	BE352290 894059C02
3	202	30.6	646	13	BW280429	BW280429 BW280429
4	202	30.6	653	13	BW280674	BW280674 BW280674
5	200	30.3	540	12	BP026060	BP026060 BP026060
6	200	30.3	541	9	AY964246	AY964246 AV964246
7	200	30.3	565	13	BW215694	BW215694 BW215694
8	200	30.3	576	12	BP013658	BP013658 BP013658
9	200	30.3	670	12	BP008971	BP008971 BP008971
10	200	30.3	680	13	BW298785	BW298785 BW298785
11	200	30.3	683	13	BW313621	BW313621 BW313621
12	200	30.3	715	13	BW079944	BW079944 BW079944
13	200	30.3	719	13	BW168960	BW168960 BW168960
14	200	30.3	720	13	BW077451	BW077451 BW077451
15	200	30.3	755	13	BW213159	BW213159 BW213159
16	200	30.3	758	9	AV897763	AV897763 AV897763
17	200	30.3	759	13	BW312507	BW312507 BW312507
18	198	30.0	615	13	BQ393735	BQ393735 NISC_0905
19	198	30.0	619	9	AL791937	AL791937 AL791937
20	198	30.0	629	9	AL649467	AL649467 AL649467
21	198	30.0	640	9	AL637277	AL637277 AL637277
22	197	29.9	418	13	BY635126	BY635126 BY635126
23	197	29.8	715	13	BW150890	BW150890 BW150890
24	196	29.7	633	13	BW286181	BW286181 BW286181
25	196	29.7	661	9	AV899426	AV899426 AV899426
26	196	29.7	674	13	BW248613	BW248613 BW248613
27	196	29.7	718	13	BW156639	BW156639 BW156639
28	196	29.7	742	13	BW117926	BW117926 BW117926
29	195	29.5	548	12	BJ064012	BJ064012 BJ064012
30	195	29.5	609	9	AW645594	AW645594 cm54f10.w
31	195	29.5	917	10	BE884392	BE884392 601505670
32	194.5	29.4	427	9	AI703692	AI703692 UI-R-ABI-
33	194.5	29.4	429	10	BE196900	BE196900 ug64h07.x
34	194.5	29.4	431	13	BY438168	BY438168 BY438168
35	194.5	29.4	432	9	AW533561	AW533561 UI-R-BUO-
36	194.5	29.4	434	12	BI289218	BI289218 UI-R-DK0-
37	194.5	29.4	454	10	BE132868	BE132868 uf37b12.x
38	194.5	29.4	463	9	AI256584	AI256584 ui88c05.x
39	194.5	29.4	467	9	AI170881	AI170881 EST216822
40	194.5	29.4	474	12	BM876762	BM876762 ih70c01.x
41	194.5	29.4	517	13	BQ208726	BQ208726 UI-R-DY1-
42	194.5	29.4	539	13	BQ174785	BQ174785 UI-M-DJ2-
43	194.5	29.4	573	9	AW553522	AW553522 L0228C10-
44	194.5	29.4	615	13	BU961938	BU961938 AGENCOURT
45	194.5	29.4	633	14	CA977210	CA977210 AGENCOURT
46	194.5	29.4	672	13	BQ209888	BQ209888 UI-R-EP0-
47	194.5	29.4	687	10	BG070290	BG070290 H3085G04-
48	194.5	29.4	691	12	BM940927	BM940927 UI-M-CG0p
49	194.5	29.4	707	13	BQ177222	BQ177222 UI-M-DJ2-
50	194.5	29.4	775	10	BG074519	BG074519 H3136B04-
51	194.5	29.4	785	10	BK083210	BK083210 H3085G04-
52	194.5	29.4	803	11	AK002397	AK002397 Mus muscu
53	194	29.3	391	10	BE626846	BE626846 ut88d02.x
54	194	29.3	394	10	AW986260	AW986260 uf76e04.x
55	194	29.3	448	12	BM876815	BM876815 ih71c02.x
56	194	29.3	464	13	EX274751	EX274751 BX274751
57	194	29.3	553	12	BM894690	BM894690 ih70c01.y
58	194	29.3	614	10	BG711517	BG711517 pg11n.pk0
59	194	29.3	614	13	BU347180	BU347180 60417259
60	194	29.3	643	13	BX259785	BX259785 BX259785
61	194	29.3	657	9	AV882930	AV882930 AV882930
62	194	29.3	696	13	BU409809	BU409809 603159073

```

63 194 29.3 698 13 BX260830
64 194 29.3 728 13 BU490085
65 194 29.3 732 13 BU115257
66 194 29.3 742 13 BU346945
67 194 29.3 752 13 BU414994
68 194 29.3 758 13 BU357913
69 194 29.3 768 13 BU312690
70 194 29.3 779 13 BU236505
71 194 29.3 779 13 BU415270
72 194 29.3 786 10 BU087149
73 194 29.3 792 13 BU108921
74 194 29.3 794 13 BU357203
75 194 29.3 795 13 BU127813
76 194 29.3 804 13 BU307748
77 194 29.3 807 13 BU107889
78 194 29.3 808 13 BU397453
79 194 29.3 922 13 BU458001
80 193 29.2 422 10 BG101052
81 193 29.2 776 13 BU303614
82 192.5 29.1 428 10 BU789469
83 192 29.0 391 10 BF075390
84 192 29.0 446 9 AV597208
85 192 29.0 457 9 AA099304
86 192 29.0 461 9 AA273692
87 192 29.0 499 14 CA941070
88 192 29.0 553 10 BF075374
89 192 29.0 611 12 BI713151
90 192 29.0 626 13 BQ632674
91 192 29.0 750 13 BX099677
92 192 29.0 876 13 BX413118
93 192 29.0 922 13 BU914040
94 191 28.9 495 14 N40217
95 191 28.9 510 13 BU074070
96 191 28.9 513 12 BJ029640
97 191 28.9 531 10 BF075368
98 191 28.9 647 14 CA381325
99 191 28.9 649 13 BU077234
100 191 28.9 1050 13 BX419276

```

ALIGNMENTS

```

RESULT 1
AV392837 466 bp mRNA linear EST 23-APR-2002
LOCUS AV392837 Chlamydomonas reinhardtii C9 Chlamydomonas reinhardtii
DEFINITION AV392837 cDNA clone CM100a09_r 5', mRNA sequence.
ACCESSION AV392837.1 GI:6547053
VERSION AV392837.1
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii
ORGANISM Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaeae; Chlamydomonas.

```

```

REFERENCE
AUTHORS Asamizu,E., Nakamura,Y., Sato,S., Fukuzawa,H. and Tabata,S.
TITLE A large scale structural analysis of cDNAs in a unicellular green
JOURNAL alga, Chlamydomonas reinhardtii. I. Generation of 3433
MEDLINE non-redundant expressed sequence tags
PUBMED DNA Res. 6 (6), 369-373 (1999)
COMMENT Contact: Yasukazu Nakamura
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakam@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
1..466
/organism="Chlamydomonas reinhardtii"
/mol_type="mRNA"
/strain="C9"
/db_xref="taxon:3055"

```

```

FEATURES
SOURCE

```

```

/clone="CM100a09_r"
/dev_stage="photoautotrophic growth"
/clone_lib="Chlamydomonas reinhardtii C9"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT 139 a 106 c 134 g 87 t
ORIGIN
Alignment Scores:
Pred. No.: 1..15e-40 Length: 466
Score: 577.00 Matches: 122
Percent Similarity: 99.19% Conservative: 0
Best Local Similarity: 99.19% Mismatches: 1
Query Match: 87.29% Indels: 1
DB: 9 Gaps: 0
US-09-866-582a-2 (1-135) x AV392837 (1-466)
QY 1 MetAspAlaValAspArgGlyValTyrPheAspGluAspPheHisValArgIleLeuAsp 20
98 ATGACGCGGTAGATAGAGGAGTCTACTTTGACGAGGACTTTCATGTCGCCATCTTCAT 157
21 ValAspLysTyrAsnAlaSerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsn 40
158 GTTGACAAAGTACAAATGCTTCAAGTCGCTCCAGGACACACAAATGTTTCATTAAACAAC 217
41 IleGlnAsnMetGlnGlyLeuValAspLysTyrValSerAlaIleAspGlnGlnValGlu 60
218 ATCCAAATATGCAAGCGCTCGTGGACAAGTACGTCGCCCATCGCAGGAGGTCGAG 277
61 ArgLeuGluAlaGluLysLeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSer 80
278 CGGCTAGAACTGAAAAGCTGAGGCCATTTGGCTGCGGAACCGGTTGGCTCGCTGAGC 337
81 GluGluArgLysArgLysGlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGlu 100
338 GAGGAGCGGAACGCTAAACAAAGGACGAGGCGCATGCTAGCGGAGAGGAGGAGGAG 397
101 LeuGluArgLeuGlnMetGluGlnSerLeuIleLysValLysGlyGluGlnGluLeu 120
398 CTGAGAGGCTCAAAATGGAGGAGCAGTCGCTGATCAG-GTGAAGGCGGAGGAGGAGCTC 456
QY 121 MetIleGln 123
Db 457 ATGATTCAG 465

```

```

RESULT 2
BE352290/c
LOCUS BE352290 493 bp mRNA linear EST 18-JUL-2000
DEFINITION 894059C02.xl C. reinhardtii CC-1690, normalized, Lambda Zap II
Chlamydomonas reinhardtii cDNA, mRNA sequence.
ACCESSION BE352290
VERSION BE352290.1 GI:9264143
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii
ORGANISM Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaeae; Chlamydomonas.
REFERENCE
AUTHORS Grossman,A., Davies,J., Federspiel,N., Harris,E., Lefebvre,P.,
McDermott,J.P., Silflow,C., Stern,D. and Surzycki,R.
TITLE Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants; project phase 2
JOURNAL Unpublished
COMMENT Contact: Elizabeth H. Harris
DCMB Box 91000
Duke University
Durham, NC 27708-1000, USA
Tel: 919 613 8164
Fax: 919 613 8177
Email: chlamy@duke.edu.
Location/Qualifiers

```

source

```

1. .493
/organism="Chlamydomonas reinhardtii"
/mol_type="mrna"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
II"

```

```

/note="vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
XhoI; This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from CC-1690 cells grown to
mid-log phase in TAP (acetate-containing) medium in the
light, TAP medium in the dark, HS (minimal) medium in
ambient levels of CO2 and HS medium bubbled with 5% CO2.
polyA mRNA was purified from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned into lambda
ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites.
pBluescript II SK- plasmids were excised from the lambda
ZAP clones by superinfection with ExAssist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al (1996) Genome Research 6: 791-806."

```

BASE COUNT 88 a 182 c 101 g 122 t

ORIGIN

Alignment Scores:

```

Pred. No.: 1.76e-10 Length: 493
Score: 227.00 Matches: 48
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 34.34% Indels: 0
DB: 10 Gaps: 0

```

US-09-866-582a-2 (1-135) x BE352290 (1-493)

```

Qy 88 LysGluGlnGluArgMetLeuAlaGluLysGlnGluGluArgLeuGlnMetGlu 107
Db 493 AAGGAGCAGAGCGCCATGCTAGCGGACAGACGAGGAGGCTTGAGAGGCTCCAAATGGAG 434
Qy 108 GluGlnSerLeuLeuLysValLysGlyGluGlnGluLeuMetIleGlnLysLeuSerAsp 127
Db 433 GAGCAGTGCCTGATCAAGGTGAGGGCGAGCAGGAGCTCATGATTCAGAGCTGCGGAC 374
Qy 128 SerSerSerGlyAlaAlaTyrVal 135
Db 373 ACCAGCAGCGCGCGGCATACGTG 350

```

RESULT 3

```

BW280429
LOCUS BW280429 Nori Satoh unpublished cDNA library, gonad Ciona
DEFINITION intestinalis cDNA clone cigd013n23 5', mRNA sequence.
ACCESSION BW280429
VERSION BW280429.1 GI:24861040
KEYWORDS EST.
SOURCE Ciona intestinalis

```

ORGANISM

```

Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.

```

REFERENCE

```

1 (bases 1 to 646)
Satou,Y., Shin-I,T., Kohara,Y. and Satoh,N.
Expressed genes in Ciona intestinalis (2002c)
JOURNAL Unpublished
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: saton@ascidian.zool.kyoto-u.ac.jp.

```

AUTHORS

```

TITLE Expressed genes in Ciona intestinalis (2002c)
JOURNAL Unpublished
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: saton@ascidian.zool.kyoto-u.ac.jp.

```

```

Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: saton@ascidian.zool.kyoto-u.ac.jp.

```

```

Location/Qualifiers
1. .646
/organism="Ciona intestinalis"
/mol_type="mrna"
/db_xref="taxon:7719"

```

FEATURES

source

```

1. .646
/organism="Ciona intestinalis"
/mol_type="mrna"
/db_xref="taxon:7719"

```

```

/clone="cigd013n23"
/tissue_type="gonad"
/clone_lib="Nori Satoh unpublished cDNA library, gonad"
BASE COUNT 223 a 107 c 121 g 194 t 1 others
ORIGIN

```

Alignment Scores:

```

Pred. No.: 3.12e-08 Length: 646
Score: 202.00 Matches: 41
Percent Similarity: 61.48% Conservative: 34
Best Local Similarity: 33.61% Mismatches: 47
Query Match: 30.56% Indels: 0
DB: 13 Gaps: 0

```

US-09-866-582a-2 (1-135) x BW280429 (1-646)

```

Qy 7 GlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyrAsnAla 26
Db 63 GGGCTTCATTTGACGAAGTTAAACAAGCTCAGAGCTTTTAAACACGACACTAATCAGCAG 122
Qy 27 SerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMetGlnGly 46
Db 123 ACATCTGAACCTGAAGGAATGCCAGATTCGTCTCGAAATCGCACCACCTTCAAAA 182
Qy 47 LeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAlaGluLys 66
Db 183 CTTGTTGGTAGCTTCATAGAGATGACCGCAGCANTCGCAAAAGATGTTGAAATCAGAAA 242
Qy 67 LeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLysArgLys 86
Db 243 ATGAAGGCCATCGGTTCTCTGTAACATGCTCAAGTCAATTCGCAAGCAGAGGAAATCC 302
Qy 87 GlnLysGluGlnGluArgMetLeuAlaGluLysGlnGlnGluLeuGluArgLeuGlnMet 106
Db 303 CAACAACAGTCAAGGCACTCATAGCGGAGAGAAACACAACTTGACGATTCGAATGTG 362
Qy 107 GluGluGlnSerLeuIleLysValLysGlyGluGlnGluLeuMetIleGlnLysLeuSer 126
Db 363 CAACACCAAGTCTCTAAGAAAACAAGAGGCTGAACAAGTTGAATTCATTGACCAATTC 422
Qy 127 AspSer 128
Db 423 ACTTCT 428

```

RESULT 4

```

BW280674
LOCUS BW280674 Nori Satoh unpublished cDNA library, gonad Ciona
DEFINITION intestinalis cDNA clone cigd014j07 5', mRNA sequence.
ACCESSION BW280674
VERSION BW280674.1 GI:24861285
KEYWORDS EST.
SOURCE Ciona intestinalis

```

ORGANISM

```

Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.

```

REFERENCE

```

1 (bases 1 to 653)
Satou,Y., Shin-I,T., Kohara,Y. and Satoh,N.
Expressed genes in Ciona intestinalis (2002c)
JOURNAL Unpublished
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: saton@ascidian.zool.kyoto-u.ac.jp.

```

AUTHORS

TITLE

JOURNAL

COMMENT

Contact:

Department of Zoology

Kyoto University

Sakyo-ku, Kyoto, Kyoto 606-8502, Japan

Tel: 81-75-753-4081

Fax: 81-75-705-1113

Email: saton@ascidian.zool.kyoto-u.ac.jp.

Location/Qualifiers

1. .653

/organism="Ciona intestinalis"

/mol_type="mrna"

/db_xref="taxon:7719"

/clone="cigd014j07"


```
/tissue_type="whole animal"
/dev_stage="egg"
/clone_lib="Nori Satoh unpublished cDNA library, egg"
BASE COUNT 188 a 97 c 103 g 153 t
ORIGIN
```

```
Alignment Scores:
Pred. No.: 4.02e-08 Length: 541
Score: 200.00 Matches: 41
Percent Similarity: 61.48% Conservatives: 34
Best Local Similarity: 33.61% Mismatches: 47
Query Match: 30.26% Indels: 0
DB: 9 Gaps: 0
```

US-09-866-582A-2 (1-135) x AV964246 (1-541)

```
QY 7 GlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyrAsnAla 26
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 69 GGGCTTCATTTTGACGAAGTTAAACAAGCTCAGAGTTTAAACACGACACTAATCAGCAG 128
QY 27 SerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMetGlnGly 46
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 129 ACATCTGACGAAAGAGGAATGCCGAATTCGTCGAAATCGGACCACTTTCAAAA 188
QY 47 LeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAlaGluLys 66
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 189 CTGTGTGAGCTTCATAGAAATGACCGACGCAATCGCAAAAGATGTTGAAATGAGAAA 248
QY 67 LeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLysArgLys 86
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 249 ATGAAGGCATCGGTTCTCGTAACATGCTCAAGTCAATTGCCAAGCAGAGGGAATCCAG 308
QY 87 GlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGluArgLeuGlnMet 106
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 309 CAACACAGATTGAAGCACTCATAGCGGAGAGAGAAAACACACTGACGATTTGAATGTG 368
QY 107 GluGluGlnSerLeuIleLysValLysGlyGluGlnGluLeuMetIleGlnLysLeuSer 126
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 369 CAACACCATGCTCTCAGGAAACAAGAGCGCGCAACAAAGTTGAATTCATTGACCAATTCCTCA 428
QY 127 AspSer 128
DB 429 ACTTCT 434
```

RESULT 7
BW215694
LOCUS BW215694 Nori Satoh unpublished cDNA library, EST 05-NOV-2002
DEFINITION intestinalis cDNA clone c1eg080k13 5', mRNA sequence.

ACCESSION BW215694
VERSION BW215694.1 GI:24630308

KEYWORDS EST.
SOURCE Ciona intestinalis

ORGANISM

Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cloniidae; Ciona.

REFERENCE 1 (bases 1 to 565)

AUTHORS Satoh,Y., Shin-i.T., Kohara,Y. and Satoh,N.

TITLE Expressed genes in Ciona intestinalis (2002c)

JOURNAL Unpublished

COMMENT

Contact: Nori Satoh

Department of Zoology

Kyoto University

Sakyo-ku, Kyoto, Kyoto 606-8502, Japan

Tel: 81-75-753-4081

Fax: 81-75-705-1113

Email: satoh@scid.ian.zool.kyoto-u.ac.jp.

FEATURES

Location/Qualifiers

1..565

/organism="Ciona intestinalis"

/mol_type="mRNA"

/db_xref="taxon:7719"

/clone="c1eg080k13"

```
/tissue_type="whole animal"
/dev_stage="egg"
/clone_lib="Nori Satoh unpublished cDNA library, egg"
BASE COUNT 195 a 99 c 109 g 162 t
ORIGIN
```

```
Alignment Scores:
Pred. No.: 4.16e-08 Length: 565
Score: 200.00 Matches: 41
Percent Similarity: 61.48% Conservatives: 34
Best Local Similarity: 33.61% Mismatches: 47
Query Match: 30.26% Indels: 0
DB: 13 Gaps: 0
```

US-09-866-582A-2 (1-135) x BW215694 (1-565)

```
QY 7 GlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyrAsnAla 26
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 71 GGGCTTCATTTTGACGAAGTTAAACAAGCTCAGAGTTTAAACACGACACTAATCAGCAG 130
QY 27 SerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMetGlnGly 46
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 131 ACATCTGACGAAAGAGGAATGCCGAATTCGTCGAAATCGACCACTTTCAAAA 190
QY 47 LeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAlaGluLys 66
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 191 CTGTGTGAGCTTCATAGAAATGACCGACGCAATCGCAAAAGATGTTGAAATGAGAAA 250
QY 67 LeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLysArgLys 86
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 251 ATGAAGGCATCGGTTCTCGTAACATGCTCAAGTCAATTGCCAAGCAGAGGGAATCCAG 310
QY 87 GlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGluArgLeuGlnMet 106
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 311 CAACACAGATTGAAGCACTCATAGCGGAGAGAGAAAACACACTGACGATTTGAATGTG 370
QY 107 GluGluGlnSerLeuIleLysValLysGlyGluGlnGluLeuMetIleGlnLysLeuSer 126
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 371 CAACACCATGCTCTCAGGAAACAAGAGCGCGCAACAAAGTTGAATTCATTGACCAATTCCTCA 430
QY 127 AspSer 128
DB 431 ACTTCT 436
```

RESULT 8

BW213658

LOCUS BW213658

DEFINITION

intestinalis cDNA clone c1ad57n03 5', mRNA sequence.

ACCESSION BW213658

VERSION BW213658.1 GI:19505135

KEYWORDS EST.

SOURCE Ciona intestinalis

ORGANISM

Ciona intestinalis

Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;

Phlebobranchia; Cloniidae; Ciona.

REFERENCE 1 (bases 1 to 576)

AUTHORS Satoh,N., Satou,Y., Kohara,Y. and Shin-i.T.

TITLE Expressed genes in Ciona intestinalis

JOURNAL Unpublished

COMMENT

Contact: Nori Satoh

Department of Zoology

Kyoto University

Sakyo-ku, Kyoto, Kyoto 606-8502, Japan

Tel: 81-75-753-4081

Fax: 81-75-705-1113

Email: satoh@scid.ian.zool.kyoto-u.ac.jp.

FEATURES

Location/Qualifiers

1..576

/organism="Ciona intestinalis"

/mol_type="mRNA"

/db_xref="taxon:7719"

/clone="c1ad57n03"

```

/tissue_type="whole animal"
/dev_stage="young adult"
/clone_lib="Nori Satoh unpublished cDNA library, young
adult"
BASE COUNT      201 a  99 c  109 g  166 t  1 others
ORIGIN

Alignment Scores:
Pred. No.:      4.23e-08      Length:      576
Score:          200.00      Matches:      41
Percent Similarity: 61.48%      Conservative: 34
Best Local Similarity: 33.61%      Mismatches:  47
Query Match:     30.26%      Indels:      0
DB:              12          Gaps:          0

US-09-866-582A-2 (1-135) x BP013658 (1-576)

QY  7 GlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyrAsnAla 26
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  52 GGCCTTCATTTGACCAAGTTTAAACAGCTCAGAGTTTAAACCAAGACACATAATCAGCAG 111
QY  27 SerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMetGlnGly 46
    ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  112 ACATCTGAACCTGAAGAGGAATGCCAGGAATTCGTCTCGAANAATCACCAGTTTCAAAA 171
QY  47 LeuValAspLysTyrValSerAlaIleAspGlnValGluArgLeuGluAlaGluLys 66
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  172 CTGTGTGGTAGCTTCATAGAAATGACCGACACAATCGCAAAAAGATGTTCAAAATGAGAAA 231
QY  67 LeuLysAlaIleGlyLeuArgMetLeuAlaGluLysGlnGluLeuGluArgLeuGlnMet 106
    ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  232 ATGAAGCCATCGGTCTCGTACATGCTCAAGTCAATTCGCAAGCAGAGGAATCCCGAG 291
QY  87 GlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluLeuGluArgLeuGlnMet 106
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  292 CAACAACAGCTGAAAGCACTCATAGCGGAGAGAGAAAACACAACACTTGAGCGATTGAATGTG 351
QY  107 GluGluGlnSerLeuIleLysValLysGlyGluGlnGluLeuMetIleGlnLysLeuSer 126
    ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  352 CAACACCACTCTCTGAGGAACAAGAGCCGCAACAAGTTGAATTATTGACCAATTCCTCA 411
QY  127 AspSer 128
    |||
Db  412 ACTTCT 417

RESULT 9
BP008971
LOCUS
DEFINITION
BP008971 Nori Satoh unpublished cDNA library, young adult Ciona
intestinalis cDNA clone ciad50e21 5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Ciona intestinalis
Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
1 (bases 1 to 670)
Satoh,N., Satou,Y., Kohara,Y. and Shin-I,T.
Expressed genes in Ciona intestinalis
Unpublished
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoheascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
1. .670
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"

FEATURES
source

```

```

/clone="ciad50e21"
/tissue_type="whole animal"
/dev_stage="young adult"
/clone_lib="Nori Satoh unpublished cDNA library, young
adult"
BASE COUNT      234 a  108 c  118 g  209 t  1 others
ORIGIN

Alignment Scores:
Pred. No.:      4.78e-08      Length:      670
Score:          200.00      Matches:      41
Percent Similarity: 61.48%      Conservative: 34
Best Local Similarity: 33.61%      Mismatches:  47
Query Match:     30.26%      Indels:      0
DB:              12          Gaps:          0

US-09-866-582A-2 (1-135) x BP008971 (1-670)

QY  7 GlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyrAsnAla 26
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  67 GGCCTTCATTTGACCAAGTTTAAACAGCTCAGAGTTTAAACCAAGACACATAATCAGCAG 126
QY  27 SerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMetGlnGly 46
    ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  127 ACATCTGAACCTGAAGAGGAATGCCAGGAATTCGTCTCGAANAATCACCAGTTTCAAAA 186
QY  47 LeuValAspLysTyrValSerAlaIleAspGlnValGluArgLeuGluAlaGluLys 66
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  187 CTGTGTGGTAGCTTCATAGAAATGACCGACACAATCGCAAAAAGATGTTCAAAATGAGAAA 246
QY  67 LeuLysAlaIleGlyLeuArgMetLeuAlaGluLysGlnGluLeuGluArgLeuGlnMet 106
    ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  247 ATGAAGCCATCGGTCTCGTACATGCTCAAGTCAATTCGCAAGCAGAGGAATCCCGAG 306
QY  87 GlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluLeuGluArgLeuGlnMet 106
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  307 CAACAACAGCTGAAAGCACTCATAGCGGAGAGAGAAAACACAACACTTGAGCGATTGAATGTG 366
QY  107 GluGluGlnSerLeuIleLysValLysGlyGluGlnGluLeuMetIleGlnLysLeuSer 126
    ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  367 CAACACCACTCTCTGAGGAACAAGAGCCGCAACAAGTTGAATTATTGACCAATTCCTCA 426
QY  127 AspSer 128
    |||
Db  427 ACTTCT 432

RESULT 10
BP008971
LOCUS
DEFINITION
BP008971 Nori Satoh unpublished cDNA library, neural complex Ciona
intestinalis cDNA clone cinc003m02 5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Ciona intestinalis
Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
1 (bases 1 to 680)
Satou,Y., Shin-I,T., Kohara,Y. and Satoh,N.
Expressed genes in Ciona intestinalis (2002c)
Unpublished
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoheascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
1. .680
/organism="Ciona intestinalis"
/mol_type="mRNA"

FEATURES
source

```

```
/db_xref="taxon:7719"
/clone="cinc003m02"
/tissue_type="neural complex"
/clone_lib="Nori Satoh unpublished cDNA library, neural complex"
BASE COUNT      245 a 107 c 120 g 208 t
ORIGIN

Alignment Scores:
Pred. No.:      4.84e-08      Length:      680
Score:          200.00      Matches:      41
Percent Similarity: 61.48%      Conservative: 41
Best Local Similarity: 33.61%      Mismatches: 47
Query Match:      30.26%      Indels:      0
DB:              13          Gaps:          0

US-09-866-582A-2 (1-135) x BW298785 (1-680)
Qy 7 GlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyrAsnAla 26
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 52 GGGCTTCATTTTGACGAAGTTAAACAAGCTCAGAGCTTTTAAACACGACACTAATCAGCAG 111
Qy 27 SerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMetGlnGly 46
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 112 ACATCTGAACCTGAAGAGGAATGCCAGCAATTCGTCGAAATCGACCACTTTCAAAA 171
Qy 47 LeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAlaGluLys 66
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 172 CTTGTTGGTAGCTTCATAGAGATGACCGACCAATCGCAAAAGATGTTGAAATGAGAAA 231
Qy 67 LeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLysArgLys 86
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 232 ATGAAAGCCATCGGTTCTCGTAACATGCTCAAGTCAATTCGCAAGCAGAGGGAATCCAG 291
Qy 87 GlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGluLeuGluArgLeuGlnMet 106
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 292 CAACAACAGTTGAAAGCACTCATAGCGGAGAGAAACACAACTTGAGCGGATTGAATGTG 351
Qy 107 GluGluGlnSerLeuIleLysValLysGlyGluGlnGluLeuMetIleGlnLysLeuSer 126
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 352 CAACACAGTCTCTAAGAAACAGAGGCTGAACAAGTTGAATTCATTGACCAATTCCTCA 411
Qy 127 AspSer 128
   |||
Db 412 ACTTCT 417

RESULT 11
BW313621
LOCUS      BW313621 Nori Satoh unpublished cDNA library, heart Ciona
DEFINITION intestinalis cDNA clone ciht026p02 5', mRNA sequence.
ACCESSION      BW313621
VERSION        BW313621.1 GI:24894232
KEYWORDS      EST.
SOURCE        Ciona intestinalis
ORGANISM      Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
1 (bases 1 to 683)
Satou,I., Shin-I,T., Kohara,Y. and Satoh,N.
Expressed genes in Ciona intestinalis (2002c)
Unpublished
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             source
                    1..683
                        /organism="Ciona intestinalis"
                        /mol_type="mRNA"
                        /db_xref="taxon:7719"

/db_xref="taxon:7719"
/clone="ciht026p02"
/tissue_type="heart"
/clone_lib="Nori Satoh unpublished cDNA library, heart"
BASE COUNT      242 a 108 c 123 g 210 t
ORIGIN

Alignment Scores:
Pred. No.:      4.86e-08      Length:      683
Score:          200.00      Matches:      41
Percent Similarity: 61.48%      Conservative: 34
Best Local Similarity: 33.61%      Mismatches: 47
Query Match:      30.26%      Indels:      0
DB:              13          Gaps:          0

US-09-866-582A-2 (1-135) x BW313621 (1-683)
Qy 7 GlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyrAsnAla 26
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 GGGCTTCATTTTGACGAAGTTAAACAAGCTCAGAGCTTTTAAACACGACACTAATCAGCAG 122
Qy 27 SerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMetGlnGly 46
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 123 ACATCTGAACCTGAAGAGGAATGCCAGCAATTCGTCGAAATCGACCACTTTCAAAA 182
Qy 47 LeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAlaGluLys 66
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 183 CTTGTTGGTAGCTTCATAGAGATGACCGACCAATCGCAAAAGATGTTGAAATGAGAAA 242
Qy 67 LeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLysArgLys 86
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 243 ATGAAAGCCATCGGTTCTCGTAACATGCTCAAGTCAATTCGCAAGCAGAGGGAATCCAG 302
Qy 87 GlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGluLeuGluArgLeuGlnMet 106
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 303 CAACAACAGTTGAAAGCACTCATAGCGGAGAGAAACACAACTTGAGCGGATTGAATGTG 362
Qy 107 GluGluGlnSerLeuIleLysValLysGlyGluGlnGluLeuMetIleGlnLysLeuSer 126
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 363 CAACACAGTCTCTAAGAAACAGAGGCTGAACAAGTTGAATTCATTGACCAATTCCTCA 422
Qy 127 AspSer 128
   |||
Db 423 ACTTCT 428

RESULT 12
BW079944/c
LOCUS      BW079944 Nori Satoh unpublished cDNA library, egg Ciona
DEFINITION intestinalis cDNA clone rcieg080k13 3', mRNA sequence.
ACCESSION      BW079944
VERSION        BW079944.1 GI:24181356
KEYWORDS      EST.
SOURCE        Ciona intestinalis
ORGANISM      Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
1 (bases 1 to 715)
Satou,I., Shin-I,T., Kohara,Y. and Satoh,N.
Expressed genes in Ciona intestinalis (2002c)
Unpublished
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             source
                    1..715
                        /organism="Ciona intestinalis"
                        /mol_type="mRNA"
                        /db_xref="taxon:7719"
```

```

/clone="rcieg080k13"
/tissue_type="whole animal"
/dev_stage="egg"
/clone_lib="Nori Satoh unpublished cDNA library, egg"
BASE COUNT      225 a 123 c 115 g 252 t
ORIGIN

```

```

Alignment Scores:
Pred. No.:      5.04e-08      Length:      715
Score:          200.00      Matches:      41
Percent Similarity: 61.48%      Conservative: 34
Best Local Similarity: 33.61%      Mismatches: 47
Query Match:      30.26%      Indels:      0
DB:              13          Gaps:      0

```

US-09-866-582A-2 (1-135) x BW079944 (1-715)

```

Qy  7 GlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyrAsnAla 26
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  669 GGGCTTCATTTGACGAAGTTAAACAAGCTCAGAGCTTTTAAACCCAGACACTAATCAGCAG 610

Qy  27 SerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMetGlnGly 46
    :::|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  609 ACATCTGAACCTGAAGAGGAATGCCACGAATTCCTCTCGAAATCGACCAAGTTTCAAAAA 550

Qy  47 LeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAlaGluLys 66
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  549 CTTGTTGAGTTCATAGAAATGACCGCACACATCGCAAAAGATGTTGAAATGAGAAA 490

Qy  67 LeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLysArgLys 86
    ==:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  489 ATGAAGCCATCGGTTCTCGTAACATGCTCAAGTCAATTGTCGAAGCAGAGGGAATCCCG 430

Qy  87 GlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGluArgLeuGlnMet 106
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  429 CAACAACAGTGTGAAGCACTCATAGCGGAGGAAGAAACACAACTTGAGCGAATTGAATGTG 370

Qy  107 GluGluGlnSerLeuIleLysValLysGlyGluGlnGluLeuMetIleGlnLysLeuSer 126
    ::|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  369 CAACACCAAGTCTCTGAGGAACAAGAGCGCCGCAACAAGTTGAATTCATTGACCAATTCTCA 310

Qy  127 AspSer 128
    |||
Db  309 ACTTCT 304

```

```

RESULT 13
LOCUS   BW168960
DEFINITION   BW168960 Nori Satoh unpublished cDNA library, neutral complex Ciona
              intestinalis cDNA clone rcieg080k13, mRNA sequence.
ACCESSION   BW168960
VERSION     BW168960.1 GI:24526185
KEYWORDS    EST.
SOURCE      Ciona intestinalis
            Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Clonidae; Ciona.
REFERENCE   1 (bases 1 to 715)
AUTHORS    Satou,Y., Shin-I,T., Kohara,Y. and Satoh,N.
TITLE       Expressed genes in Ciona intestinalis (2002c)
JOURNAL     Unpublished
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-Ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
            Location/Qualifiers
              1..719
                /organism="Ciona intestinalis"
                /mol_type="mRNA"
                /db_xref="taxon:7719"

```

FEATURES
source

```

/clone="rcinc003m02"
/tissue_type="neural complex"
/clone_lib="Nori Satoh unpublished cDNA library, neural
complex"
BASE COUNT      226 a 124 c 110 g 259 t
ORIGIN

```

```

Alignment Scores:
Pred. No.:      5.06e-08      Length:      719
Score:          200.00      Matches:      41
Percent Similarity: 61.48%      Conservative: 34
Best Local Similarity: 33.61%      Mismatches: 47
Query Match:      30.26%      Indels:      0
DB:              13          Gaps:      0

```

US-09-866-582A-2 (1-135) x BW168960 (1-719)

```

Qy  7 GlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyrAsnAla 26
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  668 GGGCTTCATTTGACGAAGTTAAACAAGCTCAGAGCTTTTAAACCCAGACACTAATCAGCAG 609

Qy  27 SerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMetGlnGly 46
    :::|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  608 ACATCTGAACCTGAAGAGGAATGCCACGAATTCCTCTCGAAATCGACCAAGTTTCAAAAA 549

Qy  47 LeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAlaGluLys 66
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  548 CTTGTTGAGTTCATAGAGATGACCGACCAATCGCAAAAGATGTTGAAATGAGAAA 489

Qy  67 LeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLysArgLys 86
    ==:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  488 ATGAAGCCATCGGTTCTCGTAACATGCTCAAGTCAATTGTCGAAGCAGAGGGAATCCCG 429

Qy  87 GlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGluArgLeuGlnMet 106
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  428 CAACAACAGTGTGAAGCACTCATAGCGGAGGAAGAAACACAACTTGAGCGAATTGAATGTG 369

Qy  107 GluGluGlnSerLeuIleLysValLysGlyGluGlnGluLeuMetIleGlnLysLeuSer 126
    ::|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  368 CAACACCAAGTCTCTGAGGAACAAGAGCGCTGAACAGTTGAATTCATTGACCAATTCTCA 309

Qy  127 AspSer 128
    |||
Db  308 ACTTCT 303

```

```

RESULT 14
LOCUS   BW077451
DEFINITION   BW077451 Nori Satoh unpublished cDNA library, egg Ciona
              intestinalis cDNA clone rcieg072121 3', mRNA sequence.
ACCESSION   BW077451
VERSION     BW077451.1 GI:24178863
KEYWORDS    EST.
SOURCE      Ciona intestinalis
            Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Clonidae; Ciona.
REFERENCE   1 (bases 1 to 720)
AUTHORS    Satou,Y., Shin-I,T., Kohara,Y. and Satoh,N.
TITLE       Expressed genes in Ciona intestinalis (2002c)
JOURNAL     Unpublished
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-Ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
            Location/Qualifiers
              1..720
                /organism="Ciona intestinalis"
                /mol_type="mRNA"
                /db_xref="taxon:7719"

```

FEATURES
source


```

/clone="cieg072121"
/tissue_type="whole animal"
/dev_stage="egg"
/clone_lib="Nori Satoh unpublished cDNA library, egg"
BASE COUNT      224 a 124 c 112 g 260 t
ORIGIN

```

```

Alignment Scores:
Pred. No.:      5.07e-08      Length:      720
Score:          200.00      Matches:      41
Percent Similarity: 61.48%      Conservative: 34
Best Local Similarity: 33.61%      Mismatches:  47
Query Match:     30.26%      Indels:      0
DB:              13          Gaps:          0

```

US-09-866-582A-2 (1-135) x BW077451 (1-720)

```

Qy  7 GlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyrAsnAla 26
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  656 GGGCTTCATTTTGACGAAGTTAAACAAGCTCAGAGCTTTTAAACACGACACTAATCAGCAG 597

Qy  27 SerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMetGlnGly 46
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  596 ACATCTGAAGTGAAGGAGGATGCCAGATTCGTCTCGAAATCGACAGTTCACAAA 537

Qy  47 LeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAlaGluLys 66
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  536 CTTCTGTGTAGCTTCATAGAAATGACCGACGCAATCGCAAAAGATGTTGAAATGAGAAA 477

Qy  67 LeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLysArgLys 86
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  476 ATGAAGCCATCGGTTCTCTAAGTCAATGCTCAAGTTCGCAAGCAGAGGGAATCCAG 417

Qy  87 GlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluLeuGluArgLeuGlnMet 106
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  416 CAACAACAGTTGAAGCACTCATAGCGGAGAGAAACACACACTTGACCGATTGAATGTG 357

Qy  107 GluGluGlnSerLeuIleLysValLysGlyGluGlnGlnGluLeuMetIleGlnLysLeuSer 126
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  356 CAACACCAAGTCTCTGAGGAACAAGAGCGGCGCAACAAGTTGAATTCATTGACCAATTCTCA 297

Qy  127 AspSer 128
    |||
Db  296 ACTTCT 291

```

```

RESULT 15
BW213159
LOCUS      BW213159      755 bp      mRNA      linear      EST 05-NOV-2002
DEFINITION      BW213159 Nori Satoh unpublished cDNA library, egg Ciona
                  intestinalis cDNA clone cie072121 5', mRNA sequence.
ACCESSION      BW213159
VERSION        BW213159.1 GI:24627773
KEYWORDS      EST.
SOURCE        Ciona intestinalis
              Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
              Phlebobranchia; Cionidae; Ciona.
REFERENCE      1 (bases 1 to 755)
AUTHORS      Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
TITLE        Expressed genes in Ciona intestinalis (2002c)
JOURNAL      Unpublished
COMMENT      Contact: Nori Satoh
              Department of Zoology
              Kyoto University
              Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
              Tel: 81-75-753-4081
              Fax: 81-75-705-1113
              Email: satoh@ascidian.zool.kyoto-u.ac.jp.
              Location/Qualifiers
FEATURES             source
                    1..755
                    /organism="Ciona intestinalis"
                    /mol_type="mRNA"
                    /db_xref="taxon:7719"

```

```

/clone="cieg072121"
/tissue_type="whole animal"
/dev_stage="egg"
/clone_lib="Nori Satoh unpublished cDNA library, egg"
BASE COUNT      267 a 117 c 130 g 241 t
ORIGIN

```

```

Alignment Scores:
Pred. No.:      5.27e-08      Length:      755
Score:          200.00      Matches:      41
Percent Similarity: 61.48%      Conservative: 34
Best Local Similarity: 33.61%      Mismatches:  47
Query Match:     30.26%      Indels:      0
DB:              13          Gaps:          0

```

US-09-866-582A-2 (1-135) x BW213159 (1-755)

```

Qy  7 GlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyrAsnAla 26
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  76 GGGCTTCATTTTGACGAAGTTAAACAAGCTCAGAGCTTTTAAACACGACACTAATCAGCAG 135

Qy  27 SerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMetGlnGly 46
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  136 ACATCTGAAGTGAAGGAGGATGCCAGATTCGTCTCGAAATCGACAGTTCACAAA 195

Qy  47 LeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAlaGluLys 66
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  196 CTTCTGTGTAGCTTCATAGAAATGACCGACGCAATCGCAAAAGATGTTGAAATGAGAAA 255

Qy  67 LeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLysArgLys 86
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  256 ATGAAGCCATCGGTTCTCTAAGTCAATGCTCAAGTTCGCAAGCAGAGGGAATCCAG 315

Qy  87 GlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluLeuGluArgLeuGlnMet 106
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  316 CAACAACAGTTGAAGCACTCATAGCGGAGAGAAACACACACTTGACCGATTGAATGTG 375

Qy  107 GluGluGlnSerLeuIleLysValLysGlyGluGlnGlnGluLeuMetIleGlnLysLeuSer 126
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  376 CAACACCAAGTCTCTGAGGAACAAGAGCGGCGCAACAAGTTGAATTCATTGACCAATTCTCA 435

Qy  127 AspSer 128
    |||
Db  436 ACTTCT 441

```

```

RESULT 16
AV897763/c
LOCUS      AV897763      758 bp      mRNA      linear      EST 09-NOV-2001
DEFINITION      AV897763 Nori Satoh unpublished cDNA library, young adult Ciona
                  intestinalis cDNA clone rciad50e21 3', mRNA sequence.
ACCESSION      AV897763
VERSION        AV897763.1 GI:16886861
KEYWORDS      EST.
SOURCE        Ciona intestinalis
              Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
              Phlebobranchia; Cionidae; Ciona.
REFERENCE      1 (bases 1 to 758)
AUTHORS      Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
TITLE        Expressed genes in Ciona intestinalis
JOURNAL      Unpublished
COMMENT      Contact: Nori Satoh
              Department of Zoology
              Kyoto University
              Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
              Tel: 81-75-753-4081
              Fax: 81-75-705-1113
              Email: satoh@ascidian.zool.kyoto-u.ac.jp.
              Location/Qualifiers
FEATURES             source
                    1..758
                    /organism="Ciona intestinalis"
                    /mol_type="mRNA"
                    /db_xref="taxon:7719"

```

```

/db_clone="rciad50e21"
/tissue_type="whole animal"
/dev_stage="young adult"
/clone_lib="Nori Satoh unpublished cDNA library, young adult"
BASE COUNT      241 a      131 c      119 g      267 t
ORIGIN

```

```

Alignment Scores:
Pred. No.:      5,29e-08      Length:      758
Score:          200.00      Matches:      41
Percent Similarity: 61.48%      Conservative: 34
Best Local Similarity: 33.61%      Mismatches: 47
Query Match:    30.26%      Indels:      0
DB:            9      Gaps:      0

```

US-09-866-582A-2 (1-135) x AV897763 (1-758)

```

QY 7 GlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyrAsnAla 26
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 679 GGGCTTCATTTGACGAAGTTAAACAAGCTCAGAGCTTTTAAACACGACACTAATCAGCAG 620
QY 27 SerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMetGlnGly 46
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 619 ACATCTGAACCTGAAGAAGAAATGCCAGCAATTCGTCTCGAAATTCGACCACTTTCAAAA 560
QY 47 LeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAlaGluLys 66
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 559 CTTGTTGTAGCTTCATAGAATGACCGCCCAATCCGAAAGAAGATGTTGAAATGAGAAA 500
QY 67 LeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLysArgLys 86
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 499 ATGAAGCCATCGGTTCTCGTAACATGCTCAAGTCAATTGCTCAAGCAGAGGGAATCCAG 440
QY 87 GlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGluArgLeuGlnMet 106
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 439 CAACAACAGTTGAAGCACTCATAGCGGAGAAGAAACACAACTTGAGCGGATGAATGTG 380
QY 107 GluGluGlnSerLeuIleLysValLysGlyGluGlnGluLeuMetIleGlnLysLeuSer 126
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 379 CAACACCAAGTCTCTGAGGAACAAGAGCGCCGAACAAGTTGAATTCATTGACCAATTCCTCA 320
QY 127 AspSer 128
|||
Db 319 ACTTCT 314

```

```

RESULT 17
BW312507
LOCUS      BW312507      759 bp      mRNA      linear      EST 11-NOV-2002
DEFINITION      Intestinalis cDNA clone ciht023e11 5', mRNA sequence.
ACCESSION      BW312507
VERSION        BW312507.1      GI:24893118
KEYWORDS
SOURCE
ORGANISM      Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Clonidae; Ciona.
REFERENCE      1 (bases 1 to 759)
AUTHORS      Satou,Y., Shin-I,T., Kohata,Y. and Satoh,N.
TITLE      Expressed genes in Ciona intestinalis (2002c)
JOURNAL      Unpublished
COMMENT      Contact: Nori Satoh
              Department of Zoology
              Kyoto University
              Sakyo-Ku, Kyoto, Kyoto 606-8502, Japan
              Tel: 81-75-753-4081
              Fax: 81-75-705-1113
              Email: satohascidian.zool.kyoto-u.ac.jp.
              Location/Qualifiers
              1..759
              /organism="Ciona intestinalis"
              /mol_type="mRNA"

```

FEATURES
source

```

/db_xref="taxon:7719"
/clone="ciht023e11"
/tissue_type="heart"
/clone_lib="Nori Satoh unpublished cDNA library, heart"
BASE COUNT      275 a      113 c      133 g      238 t
ORIGIN

```

```

Alignment Scores:
Pred. No.:      5,29e-08      Length:      759
Score:          200.00      Matches:      41
Percent Similarity: 61.48%      Conservative: 34
Best Local Similarity: 33.61%      Mismatches: 47
Query Match:    30.26%      Indels:      0
DB:            13      Gaps:      0

```

US-09-866-582A-2 (1-135) x BW312507 (1-759)

```

QY 7 GlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyrAsnAla 26
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 54 GGGCTTCATTTGACGAAGTTAAACAAGCTCAGAGCTTTTAAACACGACACTAATCAGCAG 113
QY 27 SerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMetGlnGly 46
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 114 ACATCTGAACCTGAAGAAGAAATGCCAGCAATTCGTCTCGAAATTCGACCACTTTCAAAA 173
QY 47 LeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAlaGluLys 66
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 174 CTTGTTGTAGCTTCATAGAATGACCGCCCAATCCGAAAGAAGATGTTGAAATGAGAAA 233
QY 67 LeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLysArgLys 86
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 234 ATGAAGCCATCGGTTCTCGTAACATGCTCAAGTCAATTGCTCAAGCAGAGGGAATCCAG 293
QY 87 GlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGluArgLeuGlnMet 106
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 294 CAACAACAGTTGAAGCACTCATAGCGGAGAAGAAACACAACTTGAGCGGATGAATGTG 353
QY 107 GluGluGlnSerLeuIleLysValLysGlyGluGlnGluLeuMetIleGlnLysLeuSer 126
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 354 CAACACCAAGTCTCTGAAGAAACAAGAGCGCTCAAGTGAATTCATTGACCAATTCCTCA 413
QY 127 AspSer 128
|||
Db 414 ACTTCT 419

```

```

RESULT 18
BW393735
LOCUS      BW393735      615 bp      mRNA      linear      EST 22-MAY-2002
DEFINITION      NISC_ng05b11.y1.NICHD_XGC_Emb6 Silurana tropicalis cDNA clone
IMAGE:5382476 5', mRNA sequence.
ACCESSION      BW393735
VERSION        BW393735.1      GI:21081422
KEYWORDS
SOURCE
ORGANISM      Silurana tropicalis (western clawed frog)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodidae; Silurana.
REFERENCE      1 (bases 1 to 615)
AUTHORS      NTH-XGC http://image.llnl.gov/image/html/xenopuslib.info.shtml.
TITLE      National Institute of Child Health and Human Development, National
              Cancer Institute, Xenopus Gene Collection
JOURNAL      Unpublished
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgabs-r@mail.nih.gov
              CDNA Library Preparation:
              CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
              DNA Sequencing by: National Institutes of Health Intramural
              Sequencing Center (NISC)
              Clone distribution: NCI-CGAP clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              info@image.llnl.gov
              Plate: LLAM11974 row: C column: 21

```


[illegible]

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
Xenopodinae; Silurana.

REFERENCE
AUTHORS Huckie,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J.
TITLE Sanger xenopus tropicalis EST project 2001 (10_2001)
JOURNAL Unpublished
COMMENT Contact: Huckle E
Sanger Centre
Hinnton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: Tgas049d15.sp6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
Location/Qualifiers
1..629
/organism="Silurana tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="Tgas049d15"
/dev_stage="gastrula (stages 10-5-13 mixed)"
/lab_host="Escherichia coli XL1-blue"
/clone_lib="XGC-gastrula"
/note="vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dt primed from Sug of poly A+ RNA from stages
10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
into pCS107 with EcoRI at the 5' end and NotI at the 3'
end."

BASE COUNT 205 a 132 c 138 g 154 t

ORIGIN

Alignment Scores:
Pred. No.: 6,76e-08 Length: 629
Score: 198.00 Matches: 40
Percent Similarity: 62.30% Conservative: 36
Best Local Similarity: 32.79% Mismatches: 46
Query Match: 29.95% Indels: 0
DB: 9 Gaps: 0

US-09-866-582A-2 (1-135) x AL649467 (1-629)

Oy 5 AspArgGlyValTyPheAspGluaspPheHisValArgIleLeuaspValAspLysTyr 24
||| |||:::|||||::: |||:::|||||::: |||:::|||||::: |||
40 GATCGGGGCTTCACCTTTGATGAGCTGAACAATAATGGCATCTTGATCCAGATGTGCC 99
::: |||:::|||||::: |||:::|||||::: |||:::|||||::: |||
25 AsnAlaserLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMet 44
::: |||:::|||||::: |||:::|||||::: |||:::|||||::: |||
100 CACCAACAACAACGAATTAAAGGAGGATTCAGAGATTTTGTAGACAAAATAGGCCATTTT 159
::: |||:::|||||::: |||:::|||||::: |||:::|||||::: |||
45 GlnGlyLeuValaspLysTyrValSerAlaleaspGlnGlnValGluArGLeuGluAla 64
||| |||:::|||||::: |||:::|||||::: |||:::|||||::: |||
160 CAGAAAGTAGTGGGTGGACTTAATGAACCTGTGTATGAGCTAGCAGAAAGAACCCGAAAC 219
::: |||:::|||||::: |||:::|||||::: |||:::|||||::: |||
65 GlutylLeuLysAlatIleGlyLeuArgAsnArgValAlaLaLeuSerGluGluArgLys 84
|||:::|||||:::|||||::: |||:::|||||::: |||:::|||||::: |||
220 GAATAAATGANGCAATAGTGTCCCGGACCTATTATAATCTATAGCAAAGCAAGAGAA 2799
::: |||:::|||||::: |||:::|||||::: |||:::|||||::: |||
85 ArgLysGlnLysGlnGlnGluArgMetLeuAlaGlulysGlnGlnGluLeuGluArgLeu 104
::: |||:::|||||::: |||:::|||||::: |||:::|||||::: |||
280 GCCCAGCAGCAGCAACTGTATGCCTTAATAGCAGAGAAGAAATGCAACTAGAAAGGTAC 3399
::: |||:::|||||::: |||:::|||||::: |||:::|||||::: |||
105 GlnMetGluGlnSerLeuIleLysValLysGlyGluGlnGluLeuMetIleGlnLys 124
::: |||:::|||||::: |||:::|||||::: |||:::|||||::: |||
340 CGAATAGATACGAGGCACTGTGTAAAGTGAAGCTGAACAAAATGAATTTATTGATCAA 3999
::: |||:::|||||::: |||:::|||||::: |||:::|||||::: |||
125 LeuSer 126
:::
400 TTTPAAC 405
:::

RESULT 21
AL63727

QY 125 Leuser 126
Db 411 TTTAAAC 416

RESULT 22
BY6351126
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BY6351126 418 bp mRNA linear EST 15-DEC-2002
cDNA clone K430066M20 3', mRNA sequence.
BY6351126
EST. GI:26970308
Mus musculus (house mouse)

REFERENCE
AUTHORS

1 (bases 1 to 418)
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H.,
Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C.,
Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A.,
Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S.,
Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V., Chothia, C., Corbani,
L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest,
A., Fraser, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A.,
Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J.,
Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M.,
King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons,
P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki,
H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Pertea, G.,
Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D.,
Ramachandran, S., Ravasi, R., Reed, J. C., Reed, D. J., Reid, J., Ring,
B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C. A., Setou,
M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale,
R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y.,
Watanabe, Y., Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa,
M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A.,
Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura,
M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii,
Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata,
K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander,
B. S., Rogers, J., Birney, E. and Hayashizaki, Y.

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
12456851
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsr.riken.go.jp/
URL: http://genome.gsc.riken.go.jp/
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane,
T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A.,
Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K.,
Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami,
M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct
Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Tissues were provided by Michela Fagiolini and Takao K. Hensch (
Laboratory for Neuronal Circuit Development Brain Science Institute
RIKEN 2-1 Hirose, Wako-shi, Saitama 351-0198 Japan) whose
assistance we gratefully acknowledge.
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.

FEATURES
source
Location/Qualifiers
1. 418
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="K430066M20"
/tissue_type="visual cortex"
/clone_lib="RIKEN full-length enriched, visual cortex"
BASE COUNT 134 a 70 c 120 g 94 t
ORIGIN

Alignment Scores:
Pred. No.: 5 36e-08 Length: 418
Score: 197.50 Matches: 41
Percent Similarity: 61.83% Conservative: 40
Best Local Similarity: 31.30% Mismatches: 45
Query Match: 29.88% Indels: 5
DB: 13 Gaps: 1

US-09-866-582A-2 (1-135) x BY6351126 (1-418)

QY 5 AsPArgGlyValTyrPheAspGluAspPheHisValArgLeuLeuValAspValAspLysTyr 24
Db 10 GAGCGAGGGTGGTCAATTTTGTATGAAGTCAAGCAAGCTCGAGTGTGGACCGAGGTCAACC 69
QY 25 AsnAlaSerLysSerLeuGlnAspAsnThrAsnValPheLeuAsnAsnLeuGlnAsnMet 44
Db 70 CACGAGACTGTGAGCTCAAGGAGGAGTGTGGAAGTCTGTCATGAGCAAAATTTGCCAGTTT 129
QY 45 GlnGlyLeuValAspLysTyrValSerAlaLeuAspGlnGlnValGluArgLeuGluAla 64
Db 130 CAGAAAATTTCTGTGGTGTCTAATTTGAGCTTGTTCATCAGCTTGCCAAAAGAGCAGAGAAC 189
QY 65 GluLysLeuLysAlaLeuGlyLeuArgAsnArgValAlaLeuLeuSerGluGluArgLys 84
Db 190 GAGAAGATGAAGCCATTGTGTGCTGGAAGTCTGTCATGAGTCCATAGCGAAGCAGAGAGAA 249
QY 85 ArgLysGlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGluArgLeu 104
Db 250 GCCCAGCAGCAGCAGCTGCGAGGCCCTATAGCAAAAAGAGAGCGCAGCTAGAAAGGTAT 309
QY 105 GlnMetGluGluGlnSerLeuLeuLysValLysValLysGlyGluGln-----Glu 119
Db 310 CGGTTGAATTAAGCTTTGTGTAAAGTAGAAGCAGCAACAAATGAATTTATTGACCAA 369
QY 120 LeuMetGlnLysLeuSerAspSerSer 130
Db 370 TTTATTTTTCAGAAATGAAGTGAATAATTTTCAGT 402

RESULT 23
BW150890/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BW150890 715 bp mRNA linear EST 03-NOV-2002
BW150890 Nori Satoh unpublished cDNA library, gonad Ciona
intestinalis cDNA clone rcigd013n23 3', mRNA sequence.
BW150890
EST. GI:24508115
Ciona intestinalis
Ciona intestinalis

Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enteroglossa

Eukaryota; Metazoa; Cnidaria; Ocnoidae; Ascidacea, Enterogona
Phlebobranchia; Cionidae; Ciona.

REFERENCE 1 (bases 1 to 661)
 AUTHORS Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
 TITLE Expressed genes in Ciona intestinalis
 JOURNAL Unpublished
 COMMENT Contact: Nori Satoh
 Department of Zoology
 Kyoto University
 Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
 Tel: 81-75-753-4081
 Fax: 81-75-705-1113
 Email: satoh@ascidian.zool.kyoto-u.ac.jp.

FEATURES
 source
 1..661
 /organism="Ciona intestinalis"
 /mol_type="mRNA"
 /db_xref="taxon:7719"
 /clone="rciad74m19"
 /tissue_type="whole animal"
 /dev_stage="young adult"
 /clone_lib="Nori Satoh unpublished cDNA library, young adult"

BASE COUNT 204 a 110 c 106 g 238 t 3 others
 ORIGIN

Alignment Scores:
 Pred. No.: 1.05e-07 Length: 661
 Score: 196.00 Matches: 40
 Percent Similarity: 61.16% Conservative: 34
 Best Local Similarity: 33.06% Mismatches: 47
 Query Match: 29.65% Indels: 0
 DB: 9 Gaps: 0

US-09-866-582a-2 (1-135) x AV899426 (1-661)

Qy 8 ValTyrPheAspGluAspPheHisValArgIleLeuAspValaspLysTyrAsnAlaSer 27
 Db 659 CTTTCATTTTGACGAAGTTTANCAAGCTCAGAGCTTTTAAACACAGACACTAATCAGCAGACA 600
 Qy 28 LysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMetGlnGlyLeu 47
 Db 599 TCTGAACCTGAAGAGGAATGCCAGCAATTCGTCTCGAAATCGACCAGTTTCAAAACTT 540
 Qy 48 ValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAlaGluLysLeu 67
 Db 539 GTTGGTAGCTTCATAGAAATGACCGACGCAATCGCAAAAGATGTTGAAATGAGAAATG 480
 Qy 68 LysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLysArgLysGln 87
 Db 479 AATGCCATCGGTTCTCGTAACATGCTCAAGTCAATTCGCAAGCAGAGGGAATCCAGCAA 420
 Qy 88 LysGluGlnGluArgMetLeuAlaGluLysGlnGluLeuGluArgLeuGlnMetGlu 107
 Db 419 CAACAGTTGAAGCACTCATAGCGGAGAGAAACACAACTTGAGCGATTGAATGTCAA 360
 Qy 108 GluGlnSerLeuIleLysValLysGlyGluGlnGluLeuMetIleGlnLysLeuSerAsp 127
 Db 359 CACCACTCTCTGAGGAACAAAGAGCGCGCAACAGTTGAATTCATTGACCAATTCCTCACT 300
 Qy 128 Ser 128
 Db 299 TCT 297

RESULT 26
 BW248613
 LOCUS BW248613 674 bp mRNA linear EST 09-NOV-2002
 DEFINITION BW248613 Nori Satoh unpublished cDNA library, tailbud embryo Ciona intestinalis cDNA clone citb078f08 5', mRNA sequence.
 ACCESSION BW248613
 VERSION BW248613.1 GI:24828531
 KEYWORDS EST.
 SOURCE Ciona intestinalis
 ORGANISM Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;

Phlebobranchia; Cionidae; Ciona.
 1 (bases 1 to 674)
 AUTHORS Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
 TITLE Expressed genes in Ciona intestinalis (2002c)
 JOURNAL Unpublished
 COMMENT Contact: Nori Satoh
 Department of Zoology
 Kyoto University
 Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
 Tel: 81-75-753-4081
 Fax: 81-75-705-1113
 Email: satoh@ascidian.zool.kyoto-u.ac.jp.

FEATURES
 source
 1..674
 /organism="Ciona intestinalis"
 /mol_type="mRNA"
 /db_xref="taxon:7719"
 /clone="citb078f08"
 /tissue_type="whole animal"
 /dev_stage="tailbud embryo"
 /clone_lib="Nori Satoh unpublished cDNA library, tailbud embryo"

BASE COUNT 238 a 107 c 119 g 210 t
 ORIGIN

Alignment Scores:
 Pred. No.: 1.06e-07 Length: 674
 Score: 196.00 Matches: 40
 Percent Similarity: 61.48% Conservative: 35
 Best Local Similarity: 32.79% Mismatches: 47
 Query Match: 29.65% Indels: 0
 DB: 13 Gaps: 0

US-09-866-582a-2 (1-135) x BW248613 (1-674)

Qy 7 GlyValTyrPheAspGluAspPheHisValArgIleLeuAspValaspLysTyrAsnAla 26
 Db 65 GGGCTTCATTTTGACGAAGTTTAAACAGCTCAGAGCTTTAAACACAGACTAATCAGCAG 124
 Qy 27 SerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMetGlnGly 46
 Db 125 ACATCTGAACGAAAGAGGAATGCCAGCAATTCGTCTCGAAATCGACCAGTTTCAAAA 184
 Qy 47 LeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAlaGluLys 66
 Db 185 CTTTGTGTAGCTTCATAGAAATGACCGCAATCGCAAAAGATGTTGAAATGAGAAA 244
 Qy 67 LeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLysArgLys 86
 Db 245 ATGAAGCCATCGGTTCTCGTAACATGCTCAAGTCAATTCGCAAGCAGAGGGAATCCAG 304
 Qy 87 GlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGluArgLeuGlnMet 106
 Db 305 CAACAACTGTTGAAGCACTCATAGCGGAGAGAAACACAACTTGAGCGATTGAATGTG 364
 Qy 107 GluGluGlnSerLeuIleLysValLysGlyGluGlnGluLeuMetIleGlnLysLeuSer 126
 Db 365 CAACACCACTCTCTAAGAAACAAAGAGGCTGAACAAGTTGAATTCATTGACCAATTCCTCA 424
 Qy 127 AspSer 128
 Db 425 ACTTCT 430

RESULT 27
 BW156639/c
 LOCUS BW156639 718 bp mRNA linear EST 03-NOV-2002
 DEFINITION BW156639 Nori Satoh unpublished cDNA library, gonad Ciona intestinalis cDNA clone rcig002d11 3', mRNA sequence.
 ACCESSION BW156639
 VERSION BW156639.1 GI:24513864
 KEYWORDS EST.
 SOURCE Ciona intestinalis
 ORGANISM Ciona intestinalis

Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.

REFERENCE
1 (bases 1 to 718)
AUTHORS
Satou, Y., Shin-I, T., Kohara, Y. and Satoh, N.
TITLE
Expressed genes in *Ciona intestinalis* (2002c)
JOURNAL
Unpublished
COMMENT
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@cscid.ian.zool.kyoto-u.ac.jp.

FEATURES
source
1..718
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="rcig002d11"
/tissue_type="gonad"
/clone_lib="Nori Satoh unpublished cDNA library, gonad"
BASE COUNT 221 a 127 c 110 g 260 t
ORIGIN

Alignment Scores:
Pred. No.: 1.12e-07 Length: 718
Score: 196.00 Matches: 40
Percent Similarity: 61.48% Conservative: 35
Best Local Similarity: 32.79% Mismatches: 47
Query Match: 29.65% Indels: 0
DB: 13 Gaps: 0

US-09-866-582A-2 (1-135) x BW156639 (1-718)

Qy 7 GlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyrAsnAla 26
Db 670 GGGCTTCATTTGACGAAGTTAAACAGCTCAGAGCTTTAAACACAGAGACTAATCAGCAG 611
Qy 27 SerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMetGlnGly 46
Db 610 ACATCTGAACCTGAAAGAGGAATGCCACGAATCTGCTCGAAATCGACCACTTTCAAAA 551
Qy 47 LeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAlaGluLys 66
Db 550 CTTGTGTAGCTTCATAGAATGACCGACCAATCGCAAAAGATGTTGAAAATGAGAAA 491
Qy 67 LeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLysArgLys 86
Db 490 ATGAAGCCATCGGTTCTCGTAACATGCTCAAGTCAATGCGCAGCAGAGGGAATCCAG 431
Qy 87 GlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGluLeuGluArgLeuGlnMet 106
Db 430 CAACAACAGTTGAAAGCACTCATAGCGGAGAAGAAAACACAACCTTGAGCGATTGAATGTG 371
Qy 107 GluGluGlnSerLeuIleLysValLysGlyGluGlnGluLeuMetIleGlnLysLeuSer 126
Db 370 CAACACCAAGTCTCTAAGAAAACAAGAGGCTGAACAAGTTGAATTCAATTCACCAATTCCTCA 311
Qy 127 AspSer 128
Db 310 ACTTCT 305

RESULT 28
BW117926/c 742 bp mRNA linear EST 24-OCT-2002
LOCUS
DEFINITION
BW117926 Nori Satoh unpublished cDNA library, tailbud embryo *Ciona intestinalis* cDNA clone rcitb078f08 3', mRNA sequence.
ACCESSION
BW117926
VERSION
BW117926.1 GI:24364591
KEYWORDS
Ciona intestinalis
SOURCE
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;

Phlebobranchia; Cionidae; Ciona.
1 (bases 1 to 742)
AUTHORS
Satou, Y., Shin-I, T., Kohara, Y. and Satoh, N.
TITLE
Expressed genes in *Ciona intestinalis* (2002c)
JOURNAL
Unpublished
COMMENT
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@cscid.ian.zool.kyoto-u.ac.jp.

FEATURES
source
1..742
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="rcitb078f08"
/tissue_type="whole animal"
/dev_stage="tailbud embryo"
/clone_lib="Nori Satoh unpublished cDNA library, tailbud embryo"
BASE COUNT 233 a 130 c 114 g 265 t
ORIGIN

Alignment Scores:
Pred. No.: 1.15e-07 Length: 742
Score: 196.00 Matches: 40
Percent Similarity: 61.48% Conservative: 35
Best Local Similarity: 32.79% Mismatches: 47
Query Match: 29.65% Indels: 0
DB: 13 Gaps: 0

US-09-866-582A-2 (1-135) x BW117926 (1-742)

Qy 7 GlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyrAsnAla 26
Db 668 GGGCTTCATTTGACGAAGTTAAACAGCTCAGAGCTTTAAACACAGAGACTAATCAGCAG 609
Qy 27 SerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMetGlnGly 46
Db 608 ACATCTGAACCTGAAAGAGGAATGCCACGAATCTGCTCGAAATCGACCACTTTCAAAA 549
Qy 47 LeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAlaGluLys 66
Db 548 CTTGTGTAGCTTCATAGAATGACCGACCAATCGCAAAAGATGTTGAAAATGAGAAA 489
Qy 67 LeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLysArgLys 86
Db 488 ATGAAGCCATCGGTTCTCGTAACATGCTCAAGTCAATGCGCAGCAGAGGGAATCCAG 429
Qy 87 GlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluLeuGluArgLeuGlnMet 106
Db 428 CAACAACAGTTGAAAGCACTCATAGCGGAGAAGAAAACACAACCTTGAGCGATTGAATGTG 369
Qy 107 GluGluGlnSerLeuIleLysValLysGlyGluGlnGluLeuMetIleGlnLysLeuSer 126
Db 368 CAACACCAAGTCTCTAAGAAAACAAGAGGCTGAACAAGTTGAATTCAATTCACCAATTCCTCA 309
Qy 127 AspSer 128
Db 308 ACTTCT 303

RESULT 29
BJ064012 548 bp mRNA linear EST 07-DEC-2001
LOCUS
DEFINITION
BJ064012 NIBB Mochii normalized Xenopus tailbud library Xenopus laevis cDNA clone XL078b07 5', mRNA sequence.
ACCESSION
BJ064012
VERSION
BJ064012.1 GI:17424850
KEYWORDS
Xenopus laevis (African clawed frog)
SOURCE
ORGANISM
Xenopus laevis


```

Db      88  GAGCGGGTTCAGCTTTGATGAGCTGAACAAATTCGGTATCTTGGACCCGACGCTCC 147
      |||  |||:||||:||||| |||  |||:||||:||||| |||  |||:||||:||||| |||
Qy      25  AsnAlaSerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMet 44
      ::  |||:||||: |||:||||: |||:||||: |||  |||:||||: |||  |||:||||:
Db      148  CAGCAAAACCAACCAATTAAGAGGAGAGTCCGAGATTTTGTAGACAAAATAGGACATTTT 207
      |||  |||:||||: |||:||||: |||:||||: |||  |||:||||: |||  |||:||||:
Qy      45  GlnGlyLeuValAspLysTyValSerAlaIleAspGlnValGluArgLeuGluAla 64
      |||  |||:||||: |||:||||: |||:||||: |||  |||:||||: |||  |||:||||:
Db      208  CAGAAAGTAGTGGGTGACTAATTGAGCTTTGATGAGTGTAGCTTAAGAAACCCGAAAC 267
      |||  |||:||||: |||:||||: |||:||||: |||  |||:||||: |||  |||:||||:
Qy      65  GluLysLeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLys 84
      |||  |||:||||: |||:||||: |||:||||: |||  |||:||||: |||  |||:||||:
Db      268  GAGAAATGAAGCAATAGTGCCTGCTTAAATCTATAGCAAGCAGACAGAA 327
      |||  |||:||||: |||:||||: |||:||||: |||  |||:||||: |||  |||:||||:
Qy      85  ArgLysGlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGluArgLeu 104
      |||  |||:||||: |||:||||: |||:||||: |||  |||:||||: |||  |||:||||:
Db      328  GCCCAGCAGCAGCACTATATGCTTAAAGTGAAGCTGAGCAAAATGCAACTAGAAAGGTAC 387
      |||  |||:||||: |||:||||: |||:||||: |||  |||:||||: |||  |||:||||:
Qy      105  GlnMetGluGlnGlnSerLeuLysValLysGlyGluGlnGluLeuMetIleGlnLys 124
      |||  |||:||||: |||:||||: |||:||||: |||  |||:||||: |||  |||:||||:
Db      388  CGAATAGATACGACGCTCTGTCTAAAGTGAAGCTGAGCAAAATGAATTTATTGATCAA 447
      |||  |||:||||: |||:||||: |||:||||: |||  |||:||||: |||  |||:||||:
Qy      125  LeuSer 126
      ::
Db      448  TTTAAC 453

RESULT 31
BE884392
LOCUS ..
DEFINITION BE884392 917 bp mRNA linear EST 20-OCT-2000
        601505670F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3907361 5',
        mRNA sequence.
ACCESSION BE884392
VERSION BE884392.1 GI:10333168
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9717 row: 1 column: 18
High quality sequence stop: 642.

FEATURES
    source
        1..917
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:3907361"
            /tissue_type="leiomyosarcoma"
            /lab_host="DH10B (phage-resistant)"
            /clone_lib="NIH_MGC_71"
            /note="Organ: uterus; Vector: pCMV-SPORT6; Site:1; NotI;
            Site:2; SalI; Cloned unidirectionally. Primer: Oligo dT.
            Average insert size 2.1 kb."
BASE COUNT 274 a 203 c 244 g 196 t
ORIGIN
Alignment Scores:
Pred. No.: 1.66e-07 Length: 917
Score: 195.00 Matches: 39
Percent Similarity: 62.81%

```

```

Best Local Similarity: 32.23% Mismatches: 45
Query Match: 29.50% Indels: 0
DB: 10 Gaps: 0

US-09-866-582a-2 (1-135) x BE884392 (1-917)

Qy      4  ValAspArgGlyValTyPheAspGluAspPheHisValArgIleLeuAspValAspLys 23
      |||  |||:||||: |||:||||: |||:||||: |||  |||:||||: |||  |||:||||:
Db      105  GTGAGCAGCGGCTACACTTTGATGACTGAACAGCTGAGGCTGTGGACCCAGAGGTT 164
      |||  |||:||||: |||:||||: |||:||||: |||  |||:||||: |||  |||:||||:
Qy      24  TyrAsnAlaSerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsn 43
      ::  |||:||||: |||:||||: |||:||||: |||  |||:||||: |||  |||:||||:
Db      165  ACCCAGCAGCAGCTAGAGCTGAAGGAAGAGTCCAAAGACTTTGTGGACAAAATTTGCCAG 224
      |||  |||:||||: |||:||||: |||:||||: |||  |||:||||: |||  |||:||||:
Qy      44  MetGlnGlyLeuValAspLysTyValSerAlaIleAspGlnGlnValGluArgLeuGlu 63
      |||  |||:||||: |||:||||: |||:||||: |||  |||:||||: |||  |||:||||:
Db      225  TTTGAGAAATAGTTGGTGGTAAATGAGCTTTGTTGATCAACTTCCAAAGAACAGAA 284
      |||  |||:||||: |||:||||: |||:||||: |||  |||:||||: |||  |||:||||:
Qy      64  AlaGluLysLeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArg 83
      |||  |||:||||: |||:||||: |||:||||: |||  |||:||||: |||  |||:||||:
Db      285  AATGAAAGATGAAGCCATCGTCTCGGAACCTTGCTCAAAATCTATAGCAAGCAGAGA 344
      |||  |||:||||: |||:||||: |||:||||: |||  |||:||||: |||  |||:||||:
Qy      84  LysArgLysGlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGluArg 103
      |||  |||:||||: |||:||||: |||:||||: |||  |||:||||: |||  |||:||||:
Db      345  GAAGCTCAACAGCAGCACTTCAAGCCCTAATAGCAGAAAGAAATGTCAGCTAGAAAG 404
      |||  |||:||||: |||:||||: |||:||||: |||  |||:||||: |||  |||:||||:
Qy      104  LeuGlnMetGluGlnSerLeuLysValLysGlyGluGlnGluLeuMetIleGln 123
      |||  |||:||||: |||:||||: |||:||||: |||  |||:||||: |||  |||:||||:
Db      405  TATCGGGTTGAATATCAAGCTTTGTGTAAGTAGAAGCAGACAAATGAATTTATTGAC 464
      |||  |||:||||: |||:||||: |||:||||: |||  |||:||||: |||  |||:||||:
Qy      124  Lys 124
      ::
Db      465  CAA 467

RESULT 32
AI703692
LOCUS ..
DEFINITION AI703692 427 bp mRNA linear EST 03-JUN-1999
        UI-R-ABI-yu-h-06-0-UI.s1 UI-R-ABI Rattus norvegicus cDNA clone
        UI-R-ABI-yu-h-06-0-UI 3', mRNA sequence.
ACCESSION AI703692
VERSION AI703692.1 GI:4991592
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
REFERENCE 1 (bases 1 to 427)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
JOURNAL discovery
MEDLINE Genome Res. 6 (9), 791-806 (1996)
PUBMED 97044477
COMMENT 889548
        Contact: Soares, MB
        Coordinated Laboratory for Computational Genomics
        University of Iowa
        375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
        Tel: 319 335 8250
        Fax: 319 335 9565
        Email: bento-soares@uiowa.edu
        The sequence contained an oligo-dT track that was present in the
        oligonucleotide that was used to prime the synthesis of first
        strand cDNA and therefore this may represent a bonafide poly A
        tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
        Clones will be available through Research Genetics (www.resgen.com)
        Seq primer: M13 Forward
        POLYA=Yes.
        Location/Qualifiers
            1..427
                /organism="Rattus norvegicus"
                /mol_type="mRNA"
                /strain="Sprague-Dawley"
FEATURES
    source
        1..427
            /organism="Rattus norvegicus"
            /mol_type="mRNA"
            /strain="Sprague-Dawley"

```


KEYWORDS
SOURCE
ORGANISM

EST.
Mus musculus
Mus musculus (house mouse)

REFERENCE
AUTHORS

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 431)
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaide, I., Osato, N., Saito, R., Suzuki, H., Yamana, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chochia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawai, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shinada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shingagawa, A., Tsunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
22354683
12468851
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.go.jp/
URL: http://genome.sc.riken.go.jp/
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission.
Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.
Location/Qualifiers
1. .431
/Organism="Mus musculus"

FEATURES
source

BASE COUNT

138 a 75 c 122 g 96 t

ORIGIN

US-09-866-582A-2 (1-135) x BY438168 (1-431)

Alignment Scores:
Pred. No.: 9.96e-08 Length: 431
Score: 194.50 Matches: 40
Percent Similarity: 61.83% Conservative: 41
Best Local Similarity: 30.53% Mismatches: 45
Query Match: 29.43% Indels: 5
DB: 13 Gaps: 1

/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="1920155K14"
/tissue_type="kidney"
/dev_stage="17 days embryo"
/clone_lib="RIKEN full-length enriched, 17 days embryo kidney"

QY 5 AspArgGlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyr 24
Db 23 GAGCAGGGTGGTCAATTTGATGAACCTGCAACAGCTCGGAGTGTGGACCGAGGTCAACC 82
QY 25 AsnAlaSerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMet 44
Db 83 CAGCAGACTCTGGAGCTCAAGGAGGAGTCTGGGACAAAATGCCAGTTT 142
QY 45 GlnGlyLeuValAspLysTyrValSerAlaIleAspGlnValGluArgLeuGluAla 64
Db 143 CAGAAAATTCCTGGTGTCTAATTTGATGATCAGCTTGCACAAAGAGCAGAGAAC 202
QY 65 GluLysLeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLys 84
Db 203 GAGAGATGAGGCCATTTGCTGCGAACTTCTGAAGTCCATAGGCAAGCAGAGAGAA 262
QY 85 ArgLysGlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluLeuGluArgLeu 104
Db 263 GCCCAGCAGCAGCAGCTGCAGGCCCTCATAGCAGAAAAAGAGCAGCAGTAGAAGGTAT 322
QY 105 GlnMetGluGlnSerLeuIleLysValLysGlyGluGln-----Glu 119
Db 323 CGGTTGAATATGAAGCTTTGTGTAAGTAGACAGACAAATGAATTTATTGACCAA 382
QY 120 LeuMetIleGlnLysLeuSerAspSerSer 130
Db 383 TTTATTTTTCAGAAATGAACTGAAATTTTCACT 415

RESULT 35
AW533561/c
LOCUS
DEFINITION
UI-R-BU0-and-d-03-0-UI.s1 UI-R-BU0 Rattus norvegicus cDNA clone
UI-R-BU0-and-d-03-0-UI 3', mRNA sequence.
ACCESSION
AW533561
VERSION
AW533561.1 GI:7175975
KEYWORDS
EST.
SOURCE
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE
1 (bases 1 to 432)
AUTHORS
Bonaldo, M.F., Lennon, G. and Soares, M.B.
TITLE
Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL
Genome Res. 6 (9), 791-806 (1996)
MEDLINE
97044477
PUBMED
8889548
COMMENT
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

template preparation) comprising: a) a set of about 1,000 arrayed clones from each of the five non-normalized libraries of brain (Ct0s), heart (CS0s), kidney (CU0s), aorta (CQ0s), and placenta (CX0s). The resulting pool of approximately 5,000 clones represented about 33.3% of the final driver population. A set of about 2,000 arrayed clones from each of the five normalized libraries of brain (CT0), heart (CS0), kidney (CU0), aorta (CW0), and placenta (CX0). The resulting pool of about 10,000 clones represented about 66.6% of the final driver population.

TAG_L1B=UI-R-DK0
TAG_TISSUE=rat kidney pool
TAG_SEQ=CAAGACTGTC

BASE COUNT 92 a 114 c 71 g 157 t
ORIGIN

Alignment Scores:
Pred. No.: 1e-07 Length: 434
Score: 194.50 Matches: 40
Percent Similarity: 61.83% Conservatives: 41
Best Local Similarity: 30.53% Mismatches: 45
Query Match: 29.43% Indels: 5
DB: 12 Gaps: 1

US-09-866-582a-2 (1-135) x BI289218 (1-434)

QY 5 AspArgGlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyr 24
Db 427 GAGCAGGGCTGCATTCGATGACCTGAACAAGCTTCGGGTGTGGACCCAGAGGTACC 368
QY 25 AsnAlaSerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMet 44
Db 367 CAGCAGACCAGAGCTCAAGAGAGAGTGCAAGGACTTTGTGGACAAAATGGCCAGTTT 308
QY 45 GlnGlyLeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAla 64
Db 307 CAGAAATCGTTGGTGTCTGATTCAGCTTGTTCAGCTTGTCCAAAGAGCAGAGAAC 248
QY 65 GluLysLeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLys 84
Db 247 GAGAAATGAGGCGATTCGTCGAAACTTGTCTGAATCCATAGGAGCAGAGAGAA 188
QY 85 ArgLysGlnLysGluGlnArgMetLeuAlaGluLysGlnGluGluLeuGluArgLeu 104
Db 187 GCCCAGCAGCAGCACTCCAGCAGCTGTAGCAGAAAAGAGATGCAGCTAGAAAAGTAT 128
QY 105 GlnMetGluGluGlnSerLeuIleLysValLysGlyGluGln-----Glu 119
Db 127 CCGGTTGAATATGAAGCTTTGTGTAAGTAGAAGCAGAAACAATGAATTTATTGACCAA 68
QY 120 LeuMetIleGlnLysLeuSerAspSerSer 130
Db 67 TTTATTTTCAGAAATGAATGAAATTTTCAGT 35

RESULT 37
BEI32868/c
LOCUS
DEFINITION
u37b12.x1 Soares mammary_gland_NMLMG Mus musculus cDNA clone
IMAGE:1513535 3', similar to TR:Q61025 Q61025 HYPOTHETICAL 15.2 KD
PROTEIN. ;, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 454)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
COMMENT
Unpublished
Other_ESTs: u37b12.y1

Contact: Robert Strausberg, Ph.D.
Email: cgapb-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:940387
High quality sequence stop: 414.

FEATURES
source

1. 454
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:1513535"
/sex="female (lactating)"
/tissue_type="mammary gland"
/lab_host="DH10B"
/clone_lib="Soares mammary_gland_NMLMG"
/note="Vector: p7T3D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from mammary
gland tissue from a lactating female, and was then primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified p7T3 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 101 a 127 c 78 g 148 t
ORIGIN

Alignment Scores:
Pred. No.: 1.04e-07 Length: 454
Score: 194.50 Matches: 40
Percent Similarity: 61.83% Conservatives: 41
Best Local Similarity: 30.53% Mismatches: 45
Query Match: 29.43% Indels: 5
DB: 10 Gaps: 1

US-09-866-582a-2 (1-135) x BEI32868 (1-454)

QY 5 AspArgGlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyr 24
Db 418 GAGCAGGGCTGCATTCGATGACCTGAACAAGCTTCGGGTGTGGACCCAGAGGTACC 359
QY 25 AsnAlaSerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMet 44
Db 358 CAGCAGACTCGAGCTCAAGGAGAGTGCAAGGACTTTGTGGACAAAATGGCCAGTTT 299
QY 45 GlnGlyLeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAla 64
Db 298 CAGAAAATTTGTTGGTGTCTAATTGAGCTTGTGATCAGCTTGCCTGCAAGAGCAGAGAAC 239
QY 65 GluLysLeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLys 84
Db 238 GAGAAGATGAAGGCCATTTGGTGTGCTGCAAGGCCCTGTATAGCAGAAAAGAGCAGAGGTAT 179
QY 85 ArgLysGlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluLeuGluArgLeu 104
Db 178 GCCCAGCAGCAGCAGCTGCAGGCCCTGTATAGCAGAAAAGAGCAGAGGTAT 119
QY 105 GlnMetGluGlnSerLeuIleLysValLysGlyGluGln-----Glu 119
Db 118 CCGGTTGAATATGAAGCTTTGTGTAAGTAGAAGCAGAAACAATGAATTTATTGACCAA 59
QY 120 LeuMetIleGlnLysLeuSerAspSerSer 130
Db 58 TTTATTTTCAGAAATGAATGAAATTTTCAGT 26

RESULT 38
AI256584/c
LOCUS
DEFINITION
u188c05.x1 Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:189480 3', similar to TR:Q61025 Q61025 HYPOTHETICAL 15.2 KD
PROTEIN. ;, mRNA sequence.

ACCESSION
VERSION
AI256584
AI256584.1 GI:3864109

```

KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE
JOURNAL
COMMENT

FEATURES
source
1. .463
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:1889480"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="Sugano mouse liver mlia"
/note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
(ATGTGGCCCTTTTCTTTTCTTTT); double-stranded cDNA was
ligated to a DraIII adaptor [TGTGGCCACTG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTCTGCTCTAAAGCTGGC and 3' end
primer CGACCTGCAGCTCGACACA."
BASE COUNT 97 a 127 c 76 g 163 t
ORIGIN

Alignment Scores:
Pred. No.: 1.06e-07 Length: 463
Score: 194.50 Matches: 40
Percent Similarity: 61.83% Conservatives: 41
Best Local Similarity: 30.53% Mismatches: 45
Query Match: 29.43% Indels: 5
DB: Gaps: 1

US-09-866-582a-2 (1-135) x AI256584 (1-463)

Qy 5 AspArgGlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyr 24
Db 431 GAGCAGGGCTGCATTTTGTATGTAAGTCAACAAGCTCGAGTGTGGACCCAGAGGTACC 372

Qy 25 AsnAlaSerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMet 44
Db 371 CAGCAGACTGTGGAGCTCAAGGAGGAGTCAAGAGACTTTGTGGACAAAATTTGGCCAGTTT 312

Qy 45 GlnGlyLeuValAspLysTyrValSerAlaIleAspGlnValGluArgLeuGluAla 64
Db 311 CAGAAAATTTGTGGTCTCTAAATTGAGCTTTGTTGATCAGCTTGTCCAAAAGAGCAGAAC 252

65 GluLysLeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLys 84
251 GAGAAGATGAAGCCCATTTGTCGGAAGTCTTGTGAAGTCCATAGCAGAGAGAA 192

85 ArgLysGlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluLeuGluArgLys 104
191 GCCCAGCAGCAGCAGCTGCAGGCCCTGATAGCAGAAAAGAGCAGCAGCTAGAAAGTAT 132

105 GlnMetGluGlnGlnSerLeuIleLysValLysGlyGluGln-----Glu 119
131 CGSGTGAATATGAAGCTTTGTGTAAGTAGACAGACAAAATGAATTTATTGACCAA 72

120 LeuMetIleGlnLysLeuSerAspSerSer 130
71 TTTATTTCAGAAATGAATGAAATTTTCAGT 39

RESULT 39
AII70881/c
LOCUS
DEFINITION
EST216822 Normalized rat muscle, Bento Soares Rattus sp. cDNA clone
RMUBC92 3' end, mRNA sequence.
ACCESSION
AII70881
VERSION
AII70881.1 GI:4134559
KEYWORDS
SOURCE
ORGANISM
Rattus sp.
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 467)
AUTHORS
Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J.,
Kerlavage, A.R. and Adams, M.D.
TITLE
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
Gene Index
JOURNAL
Unpublished
COMMENT
On Oct 6, 1998 this sequence version replaced gi:3710921.
Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.
FEATURES
source
1. .467
/organism="Rattus sp."
/mol_type="mRNA"
/db_xref="taxon:10118"
/clone="RMUBC92"
/note="Organ: muscle; Vector: pT7T3Pac; Site_1: EcoRI;
Site_2: NotI"
BASE COUNT 101 a 130 c 81 g 155 t
ORIGIN

Alignment Scores:
Pred. No.: 1.06e-07 Length: 467
Score: 194.50 Matches: 40
Percent Similarity: 61.83% Conservatives: 41
Best Local Similarity: 30.53% Mismatches: 45
Query Match: 29.43% Indels: 5
DB: Gaps: 1

US-09-866-582a-2 (1-135) x AII70881 (1-467)

Qy 5 AspArgGlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyr 24
Db 409 GAGCAGGGCTGCATTTTGTATGTAAGTCAACAAGCTCGAGTGTGGACCCAGAGGTACC 350

Qy 25 AsnAlaSerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMet 44
Db 349 CAGCAGACCCAGAGCTCAAGGAGAGAGTCAAGAGACTTTGTGGACAAAATTTGGCCAGTTT 290

```



```

VERSION BU961938.1 GI:24191510
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (bases 1 to 615)
JOURNAL NIH-MGC http://mgc.nci.nih.gov/.
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jonathan Kuo, NIMH
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L12CM3080 row: o column: 12
High quality sequence stop: 540.
FEATURES
source
1. 615
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6742597"
/lab_host="DH10B (TI-phage-resistant)"
/clone_lib="NIH_MGC_159"
/note="Organ: Testicles; Vector: pDNR-LIB; Site_1: SfiI
(ggcatatggcc); Site_2: SfiI (ggccctcgcc); cDNA made
by oligo-dt priming and directionally cloned. 5' and 3'
adaptors were used in cloning as follows:
5'-AAGCAGTGGTATCAACGAGAGTGGCCATTACGCCGGG-3' and
5'-ATTCTAGGCGGAGCGCGGCACATG-dt(30)NN-3'. Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the 0.5 kb
size fraction. Library created in the laboratory of M.
Brownstein (NIMH, NIH). Note: this is a NIH_MGC Library."
BASE COUNT 163 a 113 c 182 g 130 t 27 others
ORIGIN
Alignment Scores:
Pred. No.: 1.33e-07 Length: 615
Score: 194.50 Matches: 40
Percent Similarity: 61.83% Conservatve: 41
Best Local Similarity: 30.53% Mismatches: 45
Query Match: 29.43% Indels: 5
DB: 13 Gaps: 1
US-09-866-582A-2 (1-135) x BU961938 (1-615)
Qy 5 AspArgGlyValTyrPheAspGluAspPheHisValArgIleLeuValAspLysTyr 24
Db 168 GAGCAGGGTGCATTTGTGTAAGTGAACCAAGCTCCGAGTGTGGACCCAGAGGTCAACC 227
Qy 25 AsnAlaSerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMet 44
Db 228 CAGCAGACTGTGGAGCTCAGGAGGAGTGCAAGGACTTTGTGGACAAAATGGCCAGTTT 287
Qy 45 GlnGlyLeuValAspLysTyrValSerAlaIleAspGlnValGluArgLeuGluAla 64
Db 288 CAGAAAATTTGTGTGTCTAATTGAGCTTGTTCATCAGCTTGCCAAAAGACGAGAAC 347
Qy 65 GluLysLeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLys 84
Db 348 GAGAAGATGAAGGCCATTTGTGTCGGAACCTTCGTGAAGTCCATAGCAAGCAGAGAGAA 407
Qy 85 ArgLysGlnLysGluGlnArgMetLeuAlaGluLysGlnGluGluLeuGluArgLeu 104
Db 408 GCCCAGCAGCAGCAGCTGCAGGCCCTCATAGCAGAAAAGAGACCGCAGCTAGAAAGTAT 467
Qy 105 GlnMetGluGluGlnSerLeuIleLysValLysGlyGluGln-----Glu 119

```

```

Db 468 CGGTTGAATATGAAGCTTTGTGTAAGTGAACCAAGCAGACAAAATGAATTTATTGACCAA 527
Qy 120 LeuMetIleGlnLysLeuSerAspSerSerSer 130
Db 528 TTTATTTTTCAGAAATGAACGAAAATTTTCAGT 560
RESULT 45
LOCUS CA977210 633 bp mRNA linear EST 06-JAN-2003
DEFINITION AGENCOURT_11292396 NIH_MGC_164 Mus musculus cDNA clone
IMAGE:30147961 5', mRNA sequence.
CA977210
ACCESSION CA977210.1 GI:27509864
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (bases 1 to 633)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. David Rowe and Dr. Mina
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM0066 row: b column: 02
High quality sequence stop: 633.
FEATURES
source
1. 633
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:30147961"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_164"
/note="Vector: pCMV-SPORT6.1.cdb; Site_1: EcoRV; Site_2:
NotI; Non-normalized full-length enriched library from
pooled mouse embryonic limb, maxilla and mandible, day
10.5 and 11.5 (size selected for the 0.5-1 kb fragments)
Cloned directionally, priming method: Oligo-dT. cDNA
enrichment: >1k bp, Average insert size 1.8k bp. Priming
sequence: 5'-GACTAGTTCATGATCGGAGCGGCC(T) 3'. Tissue
contributed by, David Rowe. Library constructed by ResGen,
Invitrogen Corp."
BASE COUNT 183 a 125 c 190 g 135 t
ORIGIN
Alignment Scores:
Pred. No.: 1.36e-07 Length: 633
Score: 194.50 Matches: 40
Percent Similarity: 61.83% Conservatve: 41
Best Local Similarity: 30.53% Mismatches: 45
Query Match: 29.43% Indels: 5
DB: 14 Gaps: 1
US-09-866-582A-2 (1-135) x CA977210 (1-633)
Qy 5 AspArgGlyValTyrPheAspGluAspPheHisValArgIleLeuValAspLysTyr 24
Db 205 GAGCAGGGTGCATTTGTGTAAGTGAACCAAGCTCCGAGTGTGGACCCAGAGGTCAACC 264
Qy 25 AsnAlaSerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMet 44
Db 265 CAGCAGACTGTGGAGCTCAGGAGGAGTGCAAGGACTTTGTGGACAAAATGGCCAGTTT 324
Qy 45 GlnGlyLeuValAspLysTyrValSerAlaIleAspGlnValGluArgLeuGluAla 64

```

```

Db      325 CAGAAATTTGGTGTCTAATAGCTTTGATCAGCTTGCACAAAGAGCAGAGAAC 384
Qy      65 GluLysLeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLys 84
Db      385 GAGAGATGAGGCATTTGCTCGGAATCTGCTGAAGTCCATAGGCAAGCAGAGAGAA 444
Qy      85 ArgLysGlnLysGluGlnArgMetLeuAlaGluLysGlnGluLeuGluArgLeu 104
Db      445 GCCCAGCAGCAGCAGCTGCAGGCCCTGATAGCAGAAAAGAGCAGCAGCTAGAAAGTAT 504
Qy      105 GlnMetGluGlnGlnSerLeuLysValLysGlyGluGln-----Glu 119
Db      505 CGGTTGAATGAAAGCTTTGTCTAAAGTAGAAGCAGACAAATAATTTATTGACCAA 564
Qy      120 LeuMetIleGlnLysLeuSerAspSerSer 130
Db      565 TTTATTTTTCAGAAATGAACTGAAAATTTTCAGT 597

```

RESULT 46
 BQ209888/c
 LOCUS
 DEFINITION UI-R-EP0-coe-b-22-0-UI.s1 UI-R-EP0 Rattus norvegicus cDNA clone
 UI-R-EP0-coe-b-22-0-UI 3', mRNA sequence.

ACCESSION BQ209888
 VERSION BQ209888.1 GI:20426353
 KEYWORDS EST.
 SOURCE Rattus norvegicus (Norway rat)

ORGANISM
 Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene
 discovery

JOURNAL Genome Res. 6 (9); 791-806 (1996)
 MEDLINE 9704477
 PUBMED 8889548
 COMMENT Contact: Soares, MB
 Coordinated Laboratory for Computational Genomics
 University of Iowa
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: bento-soares@uiowa.edu

The sequence contained an oligo-dT track that was present in the
 oligonucleotide that was used to prime the synthesis of first
 strand cDNA and therefore this may represent a bonafide poly A
 tail. The sequence tag present in the cDNA between the NotI site
 and the oligo-dT track served to identify it as a clone from the
 normalized duodenum library cDNA Library preparation: M.B. Soares
 Lab Clone distribution: clones will be available through Research
 Genetics (www.resgen.com)
 Seq primer: M13 Forward
 PolyA=yes.

FEATURES
 source Location/Qualifiers
 1..672
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-EP0-coe-b-22-0-UI"
 /dev_stage="ADULT"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="UI-R-EP0"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; UI-R-EP0 is a
 subtracted cDNA library constructed according to Bonaldo,
 Lennon and Soares, Genome Research, 6:791-806, 1996. First
 strand cDNA synthesis was primed with an oligo-dT primer
 containing a Not I site. Double stranded cDNA was ligated
 to an EcoR I adaptor, digested with Not I, and cloned

directionally into pT73-Pac vector. The oligonucleotide
 used to prime the synthesis of first-strand cDNA contains
 a library tag sequence that is located between the Not I
 site and the (dT)18 tail. The sequence tags for this
 library are: distal colon, GAAGTGTCTCC; osteoblast,
 AAGATATCAA; cell line R3327 5A, GGAGTAGATC; cell line
 R3327 5P, CACGTGAGAT; duodenum, TGTGTTTCAT; prostate,
 CCAGG.

TAG_LIB=UI-R-EP0
 TAG_TISSUE=duodenum
 TAG_SEQ=TGTGTTTCAT"

BASE COUNT 150 a 165 c 136 g 220 t 1 others
 ORIGIN

Alignment Scores:

Pred. No.: 1,43e-07 Length: 672
 Score: 194.50 Matches: 40
 Percent Similarity: 61.83% Conservative: 41
 Best Local Similarity: 30.53% Mismatches: 45
 Query Match: 29.43% Indels: 5
 DB: 13 Gaps: 1

US-09-866-582A-2 (1-135) x BQ209888 (1-672)

Qy 5 AspArgGlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyr 24
 Db 427 GAGCGGGGCTGCACCTTCGATGAGCTGACCAAGCTTCGGGTGTGGACCCAGAGTTACC 368
 Qy 25 AsnAlaSerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMet 44
 Db 367 CAGCAGACCACAGAGCTCAAGGAAGAGTTCGAAGGACTTTGTGGACAAATTTGCCAGCTTT 308
 Qy 45 GlnGlyLeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAla 64
 Db 307 CAGAAATCTTGGTGTCTGATTTGAGCTTGTGTGATCAGCTTCCCAAGAGCAGAGAAC 248
 Qy 65 GluLysLeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluArgLys 84
 Db 247 GAGAAATGAAGCCATTGGTGTCTGAAACTTGTGTAATCCATAGCAAGCAGAGAGAA 188
 Qy 85 ArgLysGlnLysGluGlnArgMetLeuAlaGluLysGlnGluLeuGluArgLeu 104
 Db 187 GCCCAGCAGCAGCACTGCAGGCATGATAGCAGAAAAGAGATGCGAGCTAGAAAGTAT 128
 Qy 105 GlnMetGluGlnGlnSerLeuLysValLysGlyGlyGluGln-----Glu 119
 Db 127 CGGTTCAATATCAAGCTTTGTCTAAAGTAGAAGCAGACAAATAATGAATTTATTGACCAA 68
 Qy 120 LeuMetIleGlnLysLeuSerAspSerSer 130
 Db 67 TTTATTTTTCAGAAATGAACTGAAAATTTTCAGT 35

RESULT 47

BQ070290/c
 LOCUS
 DEFINITION BQ070290 687 bp mRNA linear EST 13-JUN-2003
 H3085G04-3 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone
 H3085G04 3', mRNA sequence.

ACCESSION BQ070290.1 GI:12552859

VERSION BG070290

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 687)

AUTHORS Tanaka,T.S., Jaradat,S.A., Lim,M.K., Kargul,G.J., Wang,X., Grahovac

,M.J., Pantano,S., Sano,Y., Piao,Y., Nagaraja,R., Doi,H., Wood,W.H.

III, Becker,K.G. and Ko,M.S.H.

TITLE Genome-wide expression profiling of mid-gestation placenta and

embryo using a 15,000 mouse developmental cDNA microarray

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)

MEDLINE 20381348

PUBMED 10922068

COMMENT

Other_ESTs: H3085G04-5
 Contact: George J. Kargul
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
 Email: cdna@igsun.grc.nia.nih.gov
 This clone set has been freely distributed to the community. Please
 visit <http://igsun.grc.nia.nih.gov/cdna/15k.html> for details.
 Plate: H3085 row: G column: 04
 Seq primer: -21M13 Forward
 High quality sequence stop: 687
 POLYA-Yes.

FEATURES

source
 1. .687
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="niaEST:H3085G04-3"
 /db_xref="taxon:10090"
 /clone="H3085G04"
 /sex="Clones arrayed from a variety of cDNA libraries"
 /dev_stage="Clones arrayed from a variety of cDNA libraries"
 /lab_host="DH10B"
 /clone_lib="NIA Mouse 15K cDNA Clone Set"
 /note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; This clone is among a rearranged set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, and E12.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dT)-Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray, 2000, Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."
 BASE COUNT 145 a 174 c 136 g 232 t
 ORIGIN

Alignment Scores:

Pred. No.: 1.45e-07 Length: 687
 Score: 194.50 Matches: 40
 Percent Similarity: 61.83% Conservative: 41
 Best Local Similarity: 30.53% Mismatches: 45
 Query Match: 29.43% Indels: 5
 DB: 10 Gaps: 1

US-09-866-582a-2 (1-135) x BG070290 (1-687)

Qy 5 AspArgGlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyr 24
 Db 654 GAGCAGGGCTGCATTGTGATGAACCTGAACAGCTCCGAGTGTGGACCCAGAGGTCAACC 595
 Qy 25 AsnAlaSerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMet 44
 Db 594 CAGCAGACTGTGGAGCTCAAGGAGGAGCTGTGGACAAATTTGGCAGTGT 535
 Qy 45 GlnGlyLeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAla 64
 Db 534 CAGAAAATTGTGTGTGCTCAATTGAGCTTGTGATCAGCTTGCCAAAGAGCAGAGAAC 475
 Qy 65 GluLysLeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLys 84
 Db 474 GAGAAATGAGGCCCTTGTGCTCGGAAGTGTGTAAGTCCATGAGCGACAGAGAGAA 415

Qy 85 ArgLysGlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluLeuGluArgLeu 104
 Db 414 GCCCAGCAGCAGCAGCTGCAGCCCTGTAGCAGAAAAGAGACCAGCTAGAAAGGTAT 355
 Qy 105 GlnMetGluGluGlnSerLeuLysValLysGlyGluGln-----Glu 119
 Db 354 CGGTTGTAATGAGCTTTGTGTAAGTAGAAGCAGACAAATAATTTATTGACCAA 295
 Qy 120 LeuMetIleGlnLysLeuSerAspSerSer 130
 Db 294 TTTATTTTTCAGAAATGAACCTGAAAATTTTCAGT 262

RESULT 48

BM940927/c
 LOCUS
 DEFINITION
 UI-M-CG0p-biq-b-11-0-UI.r1.NIH_BMAP_Ret4_S2 Mus musculus cDNA clone
 UI-M-CG0p-biq-b-11-0-UI 5', mRNA sequence.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS
 TITLE
 JOURNAL
 MEDLINE
 PUBMED
 COMMENT
 1 (bases 1 to 691)
 Bonaldo,M.F., Lennon,G. and Soares,M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 Genome Res. 6 (9), 791-806 (1996)
 97044477
 8889548
 Contact: Chin, H
 National Institute of Mental Health
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
 20892-9643, USA
 Tel: 301 443 1706
 Fax: 301 443 9890
 Email: mst@mail.nih.gov
 Tissue Procurement: Dr. Xin-Yuan Fu, Yale University School of
 Medicine
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com).
 Seq primer: M13 REVERSE.

FEATURES

source
 1. .691
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UI-M-CG0p-biq-b-11-0-UI"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NIH_BMAP_Ret4_S2"
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
 polylinker. Site_1: Not I; Site_2: Eco RI; The
 NIH_BMAP_Ret4_S2 library is a subtracted library,
 ultimately derived from mouse retina tissue libraries at
 various stages of development. For a detailed description
 of the library from which this clone was derived, please
 visit our web site at brainest.eng.uiowa.edu. The tissue
 for this library was contributed by Dr. Xin-Yuan Fu, Yale
 University School of Medicine"
 BASE COUNT 158 a 185 c 148 g 199 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 1.45e-07 Length: 691
 Score: 194.50 Matches: 40
 Percent Similarity: 61.83% Conservative: 41
 Best Local Similarity: 30.53% Mismatches: 45
 Query Match: 29.43% Indels: 5

```

DB: 12 Gaps: 1
US-09-866-582A-2 (1-135) x BM940927 (1-691)
Qy 5 AspArgGlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyr 24
Db 412 GAGCAGGGCTGCTATTTGATGAACTGAACAAGCTCCGAGTGTGGACCCAGAGGTCAACC 353
Qy 25 AsnAlaSerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMet 44
Db 352 CAGCAGACTGTGGAGCTCAGGAGGAGTGAAGGACTTTGTGGACAAAATGGCCAGTAT 293
Qy 45 GlnGlyLeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAla 64
Db 292 CAGAAAATTTGTTGCTGCTAAATGAGCTTGTGATCAGCTTGCCAAAAGAGCAGAGAAC 233
Qy 65 GluLysLeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLys 84
Db 232 GAGAAGATGAAGGCCATTTGCTCGGAAGCTTGTGAAGTCCATAGCAAGCAGAGAGAA 173
Qy 85 ArgLysGlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGluArgLeu 104
Db 172 GCCCAGCAGCAGCAGCTGCGGCCCTGATAGCAGAAAAGAGAGCGCAGCTAGAAAAGTAT 113
Qy 105 GlnMetGluGluGlnSerLeuIleLysValLysGlyGluGln-----Glu 119
Db 112 CGGTTGAATATGAAGCTTTGTGTAAGTAGAAGCAGACACAAAATGAATTTATTGACCAA 53
Qy 120 LeuMetIleGlnLysLeuSerAspSerSer 130
Db 52 TTTATTTTTCAGAAATGAAGTGAATAATTCAGT 20

RESULT 49
BQ177222/c
LOCUS BQ177222 707 bp mRNA linear EST 30-APR-2002
DEFINITION UI-M-DJ2-bwa-p-16-0-UI-s1 NIH-BMAP-DJ2 Mus musculus cDNA clone
BQ177222
ACCESSION BQ177222.1 GI:20352714
VERSION 1
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 707)
Normaliztion and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
8889548
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mestr@mail.nih.gov
Tissue Procurement: Dr. Robin Davison
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 FORWARD
POLYA=Yes
Location/Qualifiers
1..707
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="UI-M-DJ2-bwa-p-16-0-UI"

```

```

/tissue_type="subfornical organ and postrema"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="NIH-BMAP-DJ2"
/notes="Organ: brain; Vector: p773-Pac (Pharmacia) with a
modified polylinker; Site_1: Ecor I; Site_2: Not I;
UI-M-DJ2 is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an Ecor I adaptor, digested
with Not I, and cloned directionally into p773-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is: GCTACATGAT, subfornical
organ and area postrema.
TAG_LIB=UI-M-DJ2
TAG_TISSUE=subfornical organ and postrema
TAG_SEQ=GCTACATGAT"
BASE COUNT 158 a 185 c 148 g 214 t 2 others
ORIGIN
Alignment Scores:
Pred. No.: 1.49e-07 Length: 707
Score: 194.50 Matches: 40
Percent Similarity: 61.83% Conservative: 41
Best Local Similarity: 30.53% Mismatches: 45
Query Match: 29.43% Indels: 5
DB: 13 Gaps: 1
US-09-866-582A-2 (1-135) x BQ177222 (1-707)
Qy 5 AspArgGlyValTyrPheAspGluAspPheHisValArgIleLeuAspValAspLysTyr 24
Db 427 GAGCAGGGCTGCTATTTGATGAACTGAACAAGCTCCGAGTGTGGACCCAGAGGTCAACC 368
Qy 25 AsnAlaSerLysSerLeuGlnAspAsnThrAsnValPheIleAsnAsnIleGlnAsnMet 44
Db 367 CAGCAGACTGTGGAGCTCAAGGAGGAGTGTGGACAAAATTTGGCCAGTAT 308
Qy 45 GlnGlyLeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAla 64
Db 307 CAGAAAATTTGTTGCTGCTAAATGAGCTTGTGATCAGCTTGCCAAAAGAGCAGAGAAC 248
Qy 65 GluLysLeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLys 84
Db 247 GAGAAGATGAAGGCCATTTGCTCGGAAGCTTGTGAAGTCCATAGCAAGCAGAGAGAA 188
Qy 85 ArgLysGlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGluArgLeu 104
Db 187 GCCCAGCAGCAGCAGCTGCGGCCCTGATAGCAGAAAAGAGAGCGCAGCTAGAAAAGTAT 128
Qy 105 GlnMetGluGluGlnSerLeuIleLysValLysGlyGluGln-----Glu 119
Db 127 CGGTTGAATATGAAGCTTTGTGTAAGTAGAAGCAGACAAAATGAATTTATTGACCAA 68
Qy 120 LeuMetIleGlnLysLeuSerAspSerSer 130
Db 67 TTTATTTTTCAGAAATGAAGTGAATAATTCAGT 35
RESULT 50
BQ074519/c
LOCUS BQ074519 775 bp mRNA linear EST 13-JUN-2003
DEFINITION H3136B04-3 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone
BQ074519
ACCESSION BQ074519
VERSION BQ074519.1 GI:12557088
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

REFERENCE 1 (bases 1 to 775)
AUTHORS Tanaka,T.S., Jaradat,S.A., Lim,M.K., Kargul,G.J., Wang,X., Grahovac
M.J., Pantano,S., Sano,Y., Piao,Y., Nagajara,R., Doi,H., Wood,W.H.
III, Becker,K.G. and Ko,M.S.H.
TITLE Genome-wide expression profiling of mid-gestation placenta and
embryo using a 15,000 mouse developmental cDNA microarray
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
MEDLINE 20381348
PUBMED 10922068
COMMENT Other ESTs: H3136B04-5
Contact: George J. Kargul
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdaelgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please
visit <http://lgsun.grc.nia.nih.gov/cDNA/15k.html> for details.
Plate: H3136 Row: B Column: 04
Seq primer: -21M13 Forward
High quality sequence stop: 775
POLYA=Yes.

FEATURES Location/Qualifiers
source 1..775
organism="Mus musculus"
mol_type="mRNA"
strain="C57BL/6J"
db_xref="niaEST:H3136B04-3"
db_xref="taxon:10090"
clone="H3136B04"
sex="Clones arrayed from a variety of cDNA libraries"
dev_stage="Clones arrayed from a variety of cDNA libraries"
libraries"
lab_host="DH10B"
clone_lib="NIA Mouse 15K cDNA Clone Set"
notes="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; This
clone is among a rearranged set of 15,247 clones from 11
embryo cDNA libraries (including preimplantation stage
embryos from unfertilized egg to blastocyst, embryonic
part of E7.5 embryos, extraembryonic part of E7.5 embryos
, and E12.5 female mesonephros/gonad) and one newborn
ovary cDNA library. Average insert size 1.5 kb. All
source libraries are cloned unidirectionally with Oligo(dT
)-Not primers. References include: (1) Genome-wide
expression profiling of mid-gestation placenta and embryo
using a 15,000 mouse developmental cDNA microarray, 2000,
Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2)
Large-scale cDNA analysis reveals phased gene expression
patterns during preimplantation mouse development, 2000,
Development, 127: 1737-1749; (3) Genome-wide mapping of
unselected transcripts from extraembryonic tissue of
7.5-day mouse embryos reveals enrichment in the t-complex
and under-representation on the X chromosome, 1998, Hum
Mol Genet 7: 1967-1978."
BASE COUNT 181 a 209 c 174 g 211 t
ORIGIN

Alignment Scores:
Pred. No.: 1.6e-07 Length: 775
Score: 194.50 Matches: 40
Percent Similarity: 61.83% Conservative: 41
Best Local Similarity: 30.53% Mismatches: 45
Query Match: 29.43% Indels: 5
DB: 10 Gaps: 1

US-09-866-582A-2 (1-135) x BG074519 (1-775)
Qy 5 AspArgGlyValTyrPheAspGluAspPheHisValArgLeuLeuAspValAspLysTyr 24
::: |||:::|||||||
Db 409 GAGCGAGGCTGTCATTTTGATGAACACAAAGCTCCGAGTGTGGACCCAGAGGTCACC 350
::: |||:::|||||||
Qy 25 AsnAlaSerLysSerLeuGlnAspAsnThrAsnValPheIleAsnIleGlnAsnMet 44
::: |||:::|||||||
Db 349 CAGCAGAGCTCTGGAGCTCAAGGAGGAGTGAAGGACTTTGTGGACAAATTTGGCCAGTTT 290
::: |||:::|||||||

Qy 45 GlnGlyLeuValAspLysTyrValSerAlaIleAspGlnGlnValGluArgLeuGluAla 64
||| ::::|
Db 289 CAGAAAATTTGTTGGTGGTCTAAATTGAGCTTCTTCATCAGCTTGCCAAAAGACAGAGAAC 230
::: ::::|
Qy 65 GluLysLeuLysAlaIleGlyLeuArgAsnArgValAlaAlaLeuSerGluGluArgLys 84
|||||:::|||||||
Db 229 GAGAAGATGAAGGCCATTGGTCTCGGAACCTTGTGAAGTCCATAGCGAAGCAGAGAGAA 170
::: ::::|
Qy 85 ArgLysGlnLysGluGlnGluArgMetLeuAlaGluLysGlnGluGluArgLeu 104
::: ::::|
Db 169 GCCCAGCAGCAGCAGCTGCAGCCCTGATAGCAGAAAAGACGACGCTAGAAAGGTAAT 110
::: ::::|
Qy 105 GlnMetGluGluGlnSerLeuIleLysValLysGlyGluGln-----Glu 119
::: ::::|
Db 109 CGGTTTGAATATGAAGCTTTTGTGTAAAGTAGAAGCAGACAAATAATGAATTTATTGGCCAA 50
::: ::::|
Qy 120 LeuMetIleGlnLysLeuSerAspSerSer 130
::: ::::|
Db 49 TTTATTTTTCAGAAATGAACCTGAAAATTTTCAGT 17
::: ::::|

Search completed: August 29, 2003, 11:12:50
Job time : 2065 secs

THIS PAGE BLANK (USPTO)